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APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548PLC1
CURRENT APPLICATION NUMBER: US/09/944,457
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: December 3, 1997
PRIOR FILING DATE: December 11, 1997
PRIOR FILING DATE: December 12, 1997
PRIOR FILING DATE: December 16, 1997
361 FTGLYCESQMGQGTRPSPTPVTPRPPRSLTLGIEPVSPTSLRVGLQRYLQGSSVQLRSLR 420
                                                                                                                                                                                                                                                                                                            301 APTWLSPTAPATEAPSPPSTAPPTVGPVPQPQDCPPSTCLNGGTCHLGTRHHLACLCPEG 360
                                                                                                                                                                             FTGLYCESQMGQGTRPSPTPVTPRPPRSLTLGIEPVSPTSLRVGLQRYLQGSSVQLRSLR 420
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PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,702
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,870
PRIOR FILING DATE: December 17, 1997
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APPLICATION NUMBER: 60/068,017
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Patent No. 6734288
GENERAL INFORMATION:
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Grimaldi, Christopher
Gurney, Austin
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Filvaroff, Ellen
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APPLICANT: Botstein, David
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Goddard, Audrey
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Napier, Mary
Roy, Margaret
Tumas, Daniel
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61 ENGITMIDASSFAGIPGIQLIDISQNQIASIRLPRILLILIDISHNSLLALEPGILDTANVE 120
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100.0%; Pred. No. 6.6e-217;
tive 0; Mismatches 0;
PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/074,086
PRIOR APPLICATION NUMBER: 60/074,086
PRIOR FILING DATE: Jehruary 9, 1998
PRIOR FILING DATE: February 9, 1998
PRIOR FILING DATE: Pebruary 9, 1998
PRIOR APPLICATION NUMBER: 60/012,945
PRIOR APPLICATION NUMBER: 60/112,945
PRIOR APPLICATION NUMBER: 60/113,296
PRIOR FILING DATE: Pebruary 22, 1998
PRIOR FILING DATE: December 12, 1998
PRIOR FILING DATE: December 12, 1998
PRIOR FILING DATE: December 1, 1998
PRIOR PELLING DATE: December 1, 1998
PRIOR APPLICATION NUMBER: 60/116,221
PRIOR APPLICATION NUMBER: 60/16,221
PRIOR APPLICATION NUMBER: PCT/US98/1918
PRIOR APPLICATION NUMBER: PCT/US98/2108
PRIOR APPLICATION NUMBER: 09/24,311
PRIOR FILING DATE: December 1, 1998
PRIOR FILING DATE: December 1, 1999
PRIOR PLING DATE: December 1, 1999
PRIOR FILING DATE: December 1, 1999
PRIOR FILING DATE: December 1, 1999
PRIOR FILING DATE: December 15, 1999
PRIOR FILING DATE: December 15, 1999
PRIOR PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR PLILING DATE: PEDRICATY 22, 2000
PRIOR APPLICATION NUMBER: PCT/US90/05411
PRIOR PLILING DATE: PEDRICATY 22, 2000
PRIOR APPLICATION NUMBER: PCT/US90/05411
PRIOR APPLICATION NUMBER: PCT/US90/05411
PRIOR PLILING DATE: December 16, 1999
PRIOR PLILING DATE: DECEMBER: PCT/US90/05411
PRIOR APPLICATION NUMBER: PCT/US90/05411
PRIOR PLILING DATE: DECEMBER: PCT/US90/0550
PRIOR PLILING DATE: DECEMBER: PCT/US90/05411
PRIOR PLILING DATE: DECEMBER: PCT/US90/0550
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APPLICATION NUMBER: PCT/US99/28409
FILING DATE: No. 6734288ember 30, 1999
APPLICATION NUMBER: PCT/US99/28313
APPLICATION NUMBER: PCT/US99/28301
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FILING DATE:
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APPLICANT: Gramaldi, Christopher
APPLICANT: Gramaldi, Christopher
APPLICANT: Gramaldi, Christopher
APPLICANT: Hillan, Kenneth
APPLICANT: Kalidarin, Ivar
APPLICANT: Napier, Mary
APPLICANT: Napier, Mary
APPLICANT: Napier, Mary
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
APPLICANTON NUMBER: 09/069, 334
PRIOR APPLICATION NUMBER: 60/069, 334
PRIOR APPLICATION NUMBER: 60/069, 425
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069, 425
PRIOR FILING DATE: December 12, 1997
PRIOR FILING DATE: December 12, 1997
PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069, 694
PRIOR FILING DATE: December 16, 1997
RPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPFNCVCPLSWFGPWVRE 240
                                                                                                                              SHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSL 300
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Patent No. 6908993
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Grimaldi, Christopher
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Filvaroff, Ellen
Gerritsen, Mary
Goddard, Audrey
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APPLICANT: Botstein, David
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ENGITMIDASSPAGLPGLOLLDLSQNQIASLRLPRLILLDLSHNSLLALEPG1LDTANVE 120
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                                                                                                                                                                                                   181 RPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPFNCVCPLSWFGPWVRE 240
                                                                                                                                                                                                                      FTGLYCESQMGQGTRPSPTPVTPRPPRSLTLGIEPVSPTSLRVGLQRYLQGSSVQLRSLR 420
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                                                                                                                                121 ALRLAGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLRGLTRLRLAGNTRIAQL 180
                                                                                                                                                     241 SHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSL 300
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541 GPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGPGLQSPLHAKPYI 598
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CURRENT APPLICATION NUMBRE: US/09/944,944

CURRENT FILING DATE: 2001-09-26

PRIOR FILING DATE: 09/866,028

PRIOR FILING DATE: 09/067,411

PRIOR FILING DATE: December 3, 1997

PRIOR FILING DATE: 60/069,334

PRIOR FILING DATE: 60/069,334

PRIOR FILING DATE: 00/069,334

PRIOR FILING DATE: 00/069,334
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; Patent No. 6929947
; GENERAL INFORMATION:
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Grimaldi, Christopher
Gurney, Austin
Hillan, Kenneth
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Gerritsen, Mary
Goddard, Audrey
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APPLICANT: Botstein, David
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Napier, Mary
Roy, Margaret
Tumas, Daniel
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RION APPLICATION NUMBER: 60/66,278
RRIOR APPLICATION NUMBER: 60/66,284
RRIOR APPLICATION NUMBER: 60/66,694
RRIOR PRILING DATE: December 16, 1997
RRIOR APPLICATION NUMBER: 60/66,694
RRIOR PELING DATE: December 16, 1997
RRIOR APPLICATION NUMBER: 60/66,694
RRIOR FILING DATE: December 16, 1997
RRIOR PELING DATE: DECEMBER 16, 1997
RRIOR PELING DATE: DECEMBER 16, 1997
RRIOR PELING DATE: DECEMBER 17, 1997
RRIOR PELING DATE: DECEMBER 17, 1997
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RRIOR PELING DATE: DECEMBER 16, 1997
RRIOR PELING DATE: DECEMBER 16, 1997
RRIOR APPLICATION NUMBER: 60/00,440
RRIOR APPLICATION NUMBER: 60/00,440
RRIOR APPLICATION NUMBER: 60/104,986
RRIOR RILING DATE: FEBRUARY 5, 1998
RRIOR RELING DATE: FEBRUARY 5, 1998
RRIOR PELING DATE: FEBRUARY 5, 1998
RRIOR PELING DATE: FEBRUARY 5, 1998
RRIOR PELING DATE: FEBRUARY 60/104,092
RRIOR PELING DATE: FEBRUARY 5, 1998
RRIOR PELING DATE: FEBRUARY 5, 1998
RRIOR PELING DATE: SEPEMBER: 60/116, 222
RRIOR PELING DATE: BECEMBER: 61, 1998
RRIOR APPLICATION NUMBER: PCT/US99/12851
RRIOR APPLICATION NUMBER: PCT/US99/12851
RRIOR APPLICATION NUMBER: PCT/US99/12851
RRIOR APPLICATION NUMBER: PCT/US99/12865
RRIOR APPLICATION NUMBER: PCT/US99/12865
RRIOR APPLICATION NUMBER: PCT/US99/12865
RRIOR APPLICATION NUMBER: PCT/US99/12861
RRIOR APPLICATION NUMBER: PCT/US99/12
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                                                                                                                              1 MCSRVPLLLPLLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLVVF 60
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APPLICANT: Tumes, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/945,587
                                                                                             Gaps
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                                                    Query Match 100.0%; Score 3135; DB 2; Length 598; Best Local Similarity 100.0%; Pred. No. 6.6e-217; Matches 598; Conservative 0; Mismatches 0; Indels 0
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Patent No. 693654
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botestein, David
APPLICANT: Faton, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Ferrara, Napoleone
APPLICANT: Forriten, Mary
APPLICANT: Goddwaki, Paul
APPLICANT: Goddwaki, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Grimaldi, Christopher
APPLICANT: Glanaldi, Christopher
APPLICANT: Hillan, Kenneth
APPLICANT: Hillan, Kenneth
APPLICANT: Napier, Mary
APPLICANT: Napier, Mary
; ORGANISM: Homo Sapien
US-09-944-944-69
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PRIOR APPLICATION NUMBER: 09/866,028
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR APPLICATION NUMBER: 60/669334
PRIOR APPLICATION NUMBER: 60/669334
PRIOR APPLICATION NUMBER: 60/669334
PRIOR APPLICATION NUMBER: 60/669315
PRIOR APPLICATION NUMBER: 60/669122
PRIOR APPLICATION NUMBER: 60/669122
PRIOR PILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/669, 634
PRIOR APPLICATION NUMBER: 60/69, 639
PRIOR APPLICATION NUMBER: 60/10440
PRIOR PILING DATE: December 11, 1998
PRIOR PILING DATE: December 21, 1998
PRIOR PILING DATE: SEPECAMER 90/126, 021
PRIOR PILING DATE: SEPECAMER 10/1299
PRIOR PILING DATE: SEPECAMER 11/1299
PRIOR PILING DATE: PENCAMER: PCT/US99/2009
PRIOR PILING DATE
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    US-09-063-950-2
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Sequence 2, Application US/09063950C

Sequence 2, Application US/09063950C

Patent No. 6225085

GENERAL NO. 6225085

TITLE OF INVENTION: THEREPOR

TITLE OF INVENTION: THEREPOR

TITLE OF INVENTION: THEREPOR

TITLE OF INVENTION UNMBER: US/09/063,950C

CURRENT APPLICATION NUMBER: US/09/063,950C

CURRENT APPLICATION NUMBER: US/09/063,950C

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 2

LENGTH: 673
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100.0%; Pred. No. 6.6e-217;
rative 0; Mismatches 0; Indels
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: Pebruary 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 69
LENGTH: 598
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ORGANISM: Homo sapiens
                                                                                           TYPE: PRT
; ORGANISM: Homo Sapien
US-09-945-587-69
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Best Local Similarity
Matches 598; Conserv
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                                                                                                                 91 ------LRLPRLLLLDLSHNS
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                                                                                         1 MCSRVPLLLPLLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVF
                                                Gaps
                                              75;
    Length 673;
                                              Indels
98.4%; Score 3083.5; DB 2;
88.7%; Pred. No. 3.8e-213;
iive 0; Mismatches 1; ]
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; Patent No. 6913919
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Grimaldi, J. Christopher
Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eaton, Dan L.
Ferrara, Napoleone
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Gerber, Hanspeter
Gerritsen, Mary E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INCORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Besetein, David
APPLICANT: Besnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerber, Hanspeter
APPLICANT: Grimaldi, J. Christ
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Laurey
APPLICANT: Godowski, Paul J.
APPLICANT: Gutney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PGLOSPLHAKPYI 598
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Best Local Similarity 88.7
Matches 597; Conservative
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APPLICANT: Watanabe, Colini K.
APPLICANT: Watanabe, Colini K.
APPLICANT: Watanabe, Colini K.
APPLICANT: Wood, Milliams P. Wickey
APPLICANT: Wood, Milliams P. Wickey
TITLE OF INVANTION: Secide Encoding the Same
CURRENT APPLICATION WORBER: 60/043797
THE STREAM APPLICATION WORBER: 60/043797
PRIOR PLILING DATE: 1397-11.15
PRIOR PLILING DATE: 1397-11.12
PRIOR PLILING DATE: 1397-11.12
PRIOR PLILING DATE: 1397-11.13
PRIOR PLILING DATE: 1397-11.13
PRIOR PLILING DATE: 1397-11.13
PRIOR PLILING DATE: 1397-11.13
PRIOR PLILING DATE: 1398-12.24
PRIOR PLILING DATE: 1398-12.24
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PRIOR APPLICATION WORBER: 60/06311
PRIOR APPLICATION WORBER: 60/06312
PRIOR APPLICATION WORBER: 60/06312
PRIOR APPLICATION WORBER: 60/06312
PRIOR APPLICATION WORBER: 60/06302
PRIOR APPLICATION WORBER: 60/06302
PRIOR APPLICATION WORBER: 60/06303
PRIOR PLILING DATE: 1398-06-04
PRIOR PLILING DATE: 1398-06-04
PRIOR APPLICATION WORBER: 60/06303
PRIOR PLILING DATE: 1398-06-04
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APPLICATION NUMBER: 60/088738
                                                                                                                                                                                               Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
                                                                                                                Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
                                                                                 Paoni, Nicholas F.
Kljavin, Ivar J.
                              Napier, Mary A.
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APPLICANT:
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PRIOR APPLICATION NUMBER: 60/08810
PRIOR FILING DATE: 1998-06-10
PRIOR FILING DATE: 1998-06-10
PRIOR FILING DATE: 1998-06-10
PRIOR PELING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/08826
PRIOR APPLICATION NUMBER: 60/08858
PRIOR PILING DATE: 1998-06-11
PRIOR PILING DATE: 1998-06-11
PRIOR PILING DATE: 1998-06-11
PRIOR PILING DATE: 1998-06-12
PRIOR PILING DATE: 1998-06-16
PRIOR PILING DATE: 1998-06-16
PRIOR PILING DATE: 1998-06-16
PRIOR PILING DATE: 1998-06-16
PRIOR PILING DATE: 1998-06-17
PRIOR PILING DATE: 1998-06-17 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088810 APPLICATION NUMBER: 60/089908 PILING DATE: 1998-06-18 APPLICATION NUMBER: 60/089908 APPLICATION NUMBER: 60/090435
APPLICATION NUMBER: 60/090435
APPLICATION PPLICATION NUMBER: 60/088742 [LING DATE: 1998-06-10 FILING DATE: 1998-06-22
APPLICATION NUMBER: 60/090254
FILING DATE: 1998-06-22
APPLICATION NUMBER: 60/090349
FILING DATE: 1998-06-23 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090540 FILING DATE: 1998-06-24 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089801 FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/089948 FILING DATE: 1998-06-19 APPLICATION NUMBER: 60/089952 APPLICATION NUMBER: 60/090429 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090431 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090445 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090535 FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/089907 FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/089947 FILING DATE: 1998-06-19 APPLICATION NUMBER: 60/090246 FILING DATE: 1998-06-22 APPLICATION NUMBER: 60/090252 FILING DATE: 1998-06-23 APPLICATION NUMBER: 60/090355 FILING DATE: 1998-06-23 FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090472 1998-06-10 FILING DATE: 1998-06-19 PRIOR PRIOR

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APPLICANT: Wood, William International Applicant: Zhang, Zemin APPLICANT: Zhang, Zemin APPLICANT: Zhang, Zemin TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2730PL09
FILE REFERENCE: P2730PL09
FILE REPERENCE: P2730PL09
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FILE REPERENCE: P2730PL09
FILE REPERENCE: P370PL09
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               121 HLGTRHHLACLCPEGFTGLYCESQMGQGTRPSPTPVTPRPPRSLTLGIEPVSPTSLRVGL 480
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Gurney, Austin L.
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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Ferrara, Napoleone
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Gerber, Hanspeter
Gerritsen, Mary E.
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Botstein, David
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US-09-990-444-52
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PRIOR APPLICATION NUMBER: 60/090542
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090557
PRIOR APPLICATION NUMBER: 60/090676
PRIOR PILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR PILING DATE: 1998-06-25
PRIOR PILING DATE: 1998-06-26
PRIOR PILING DATE: 1998-07-01
PRIOR PILING DATE: 1998-07-01
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
PRIOR PAPLICATION NUMBER: 60/09163
PRIOR PILING DATE: 1998-07-02
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Matches 597; Conser
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PRIOR APPLICATION NUMBER: 60/08769
PRIOR PLIKO DATE: 1998-06-02
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PRIOR PLIKO DATE: 1998-06-03
PRIOR PLIKO DATE: 1998-06-04
PRIOR PLIKO DATE: 1998-06-07
PRIOR PRICATION NUMBER: 60/08926
PRIOR PRICATION NUMBER: 60/08929
PRIOR PRICATION NUMBER: 60/08929
PRIOR PRICATION NUMBER: 60/08929
PRIOR PRICATION NUMBER: 60/0892

PRIOR FLIGHTON DATE: 1998-06-18
PRIOR PLING DATE: 1998-06-18
PRIOR PLING DATE: 1998-06-18
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PRIOR PLING DATE: 1998-06-19
PRIOR PLING DATE: 1998-06-12
PRIOR PLING DATE: 1998-06-22
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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PILIE OF THINGUISTON NUMBER: US/99/997,333
CURRENT APPLICATION NUMBER: US/99/997,333
CURRENT FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-10-17
PRIOR PELING DATE: 1997-10-17
PRIOR PELING DATE: 1997-11-12
PRIOR PELING DATE: 1997-11-12
PRIOR PELING DATE: 1997-11-12
PRIOR FILING DATE: 1997-11-13
PRIOR PELICATION NUMBER: 60/06536
PRIOR FILING DATE: 1997-11-13
PRIOR PELICATION NUMBER: 60/06570
PRIOR FILING DATE: 1998-02-25
PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-03-20
PRIOR PELICATION NUMBER: 60/08709
PRIOR PELICATION NUMBER: 60/08709
PRIOR PELICATION NUMBER: 60/08709
PRIOR PELING DATE: 1998-05-07
PRIOR PELICATION NUMBER: 60/08709
PRIOR PELING DATE: 1998-06-02
PRIOR PELICATION NUMBER: 60/08709
PRIOR PELING DATE: 1998-06-02
PRIOR PELICATION NUMBER: 60/08709
PRIOR PELING DATE: 1998-06-07
PRIOR PELICATION NUMBER: 60/08702
PRIOR PELING DATE: 1998-06-07
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PRIOR PELING DATE: 1998-06-07
PRIOR PELICATION NUMBER: 60/08803
PRIOR PELICA
                                                                                               Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Williams, P. Mickey
Wood, William I.
                          Kljavin, Ivar J.
Napier, Mary A.
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                                                                                                                                 Gaps
                                                                                                                            75;
                                                                       98.4%; Score 3083.5; DB 2; Length 673; 88.7%; Pred. No. 3.8e-213; ive 0; Mismatches 1; Indels 75;
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Gerritsen, Mary B.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J.Christopher
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
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Eaton, Dan L.
Ferrara, Napoleone
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APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferzara, Napoleon
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
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                                                                                               Best Local Similarity 88.7
Matches 597, Conservative
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1998-06-24

R APPLICATION NUMBER: 60/089738

R FILING DATE: 1998-06-10

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R APPLICATION NUMBER: 60/08824

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R APPLICATION NUMBER: 60/08865

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R FILING DATE: 1998-06-17

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R APPLICATION NUMBER: 60/08959 R FILING DATE: 1998-06-18
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R FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090435
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APPLICATION NUMBER: 60/090535
FILING DATE: 1998-06-24 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090445 APPLICATION NUMBER: 60/090252 FILING DATE: 1998-06-22 APPLICATION NUMBER: 60/090540 PRIOR PRIOR

121 RGLRRLERLYLGKNRIRHIQPGAFDTLDRLLELKLQDNELRALPPLRLFLLLLDLSHNS LLALEPGILDTANVEALRLAGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLRG LIALEPGILDTANVEALRLAGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLRG LTRIRLAGNTRI AQLR PEDLAGLAALQEL DVSNI, SLQAL PGDLSGLF PRLRLLAAARN PF NCVCPLSWFGPWVRESHVTLASPBETRCHFPPKNAGRLILLELDYADFGCPATTTTATVPT TRPVVREPTALSSSLAPTWLSPTAPATEAPSPPSTAPPTVGPVPQPQDCPPSTCLNGGTC TRPVVREPTALSSSLAPTWLSPTAPATEAPSPPSTAPPTVGPVPQPQDCPPSTCLNGGTC MCSRVPLLLPLLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVF MCSRVPLLLPLLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVF LTRLRLAGUTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPF NCVCPLSWFGPWVRESHVTLASPEETRCHFPPXNAGRLLLELDYADFGCPATTTTATVPT Gaps 75; Length 673; Indels DB 2; Score 3083.5; DB 2; Pred. No. 3.8e-213; 0; Mismatches 1; PRIOR APPLICATION NUMBER: 60/090542
PRIOR FILING DATE: 1998-06-24
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PRIOR PILING DATE: 1998-06-25
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PRIOR PELING DATE: 1998-07-01
PRIOR PELING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-07
PRIOR PELING DATE: 1998-07-07 APPLICATION NUMBER: 60/091982 FILING DATE: 1998-07-07 APPLICATION NUMBER: 60/092182 FILING DATE: 1998-07-09 Query Match
Best Local Similarity 88.7%;
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CURRENT FILING DATE: 2001-11-14

PRIOR APPLICATION NUMBER: 60/0649787

PRIOR FILING DATE: 1997-06-16

PRIOR FILING DATE: 1997-11-12

PRIOR PLICATION NUMBER: 60/065186

PRIOR APPLICATION NUMBER: 60/065311

PRIOR PLILING DATE: 1997-11-12

PRIOR APPLICATION NUMBER: 60/065311

PRIOR PLILING DATE: 1997-11-13

PRIOR PLILING DATE: 1997-11-24
                                                      481 QRYLQGSSVQLRSLRLTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCWPLGP 540
                                                                                                                                            QRYLQGSSVQLRSLRLTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCVMPLGP 465
                                                                                          GRVPEGEEACGEAHTPPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVR 525
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PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
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Godowski, Paul J.
Grimaldi, J.Christopher
Gurney, Austin L.
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
Tumas, Daniel
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Ferrara, Napoleone
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Gerritsen, Mary E.
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R APPLICATION NUMBER: 60/088738
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A APPLICATION NUMBER: 60/087607
FILING DATE: 1998-06-02
A PILING DATE: 1998-06-02
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A PAPLICATION NUMBER: 60/087759 R FILING DATE: 1998-06-02
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R FILING DATE: 1998-06-03
A APPLICATION NUMBER: 60/088021
R FILING DATE: 1998-06-04
R APPLICATION NUMBER: 60/088025
R FILING DATE: 1998-06-04 R FILING DATE: 1998-06-04
A APPLICATION WNBRER: 60/088033
A APPLICATION NUMBER: 60/088326
R FILING DATE: 1998-06-04
R PAPLICATION NUMBER: 60/088167
R FILING DATE: 1998-06-05 FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089600
FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089653
FILING DATE: 1998-06-17 FILING DATE: 1998-06-11
APPLICATION NUMBER: 60/089105
FILING DATE: 1998-06-12
APPLICATION NUMBER: 60/089440
FILING DATE: 1998-06-16 APPLICATION NUMBER: 60/088026 FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088028 FILING DATE: 1998-06-04
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PRIOR APPLICATION NUMBER: 60/08901
PRIOR PRIME LIMEO DERE: 1998-66-18
PRIOR FILLING DIRE: 1998-66-18
PRIOR PELLING DIRE: 1998-66-18
PRIOR PELLING DIRE: 1998-66-19
PRIOR PELLING DATE: 1998-66-29
PRIOR PELLING DATE: 1998-66-24
PRIOR PELLING DATE: 1998-66-25
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PRIOR PELLING DATE: 199
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Sequence 10, Application US/09520781

Patent No. 6689866

GENERAL INFORMATION:

APPLICANT: Shimkets, Richard A.

TITLE OF INVENTION: NOVEL POLYNUCLECTIDES AND PROTEINS ENCODED THEREBY

TITLE OF INVENTION: NOVEL POLYNUCLECTIDES AND PROTEINS ENCODED THEREBY

CURRENT APPLICATION NUMBER: US/09/520, 781

CURRENT APPLICATION NUMBER: US/09/520, 781

PRIOR APPLICATION NUMBER: US/09/520, 781

PRIOR FILING DATE: 1999-03-09

NUMBER OF SEQ ID NOS: 81

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 10

LENGTH: 653
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                                                                                                                                          1 MCSRVPLLLPLLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVF
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                                                                                                                     1 MCSRVPLLLPLLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVF
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                                                                                         Gaps
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                                                             DB 2;
                                                           Score 3083.5; DB 2
Pred. No. 3.8e-213;
0; Mismatches 1;
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
                                                          Query Match
Best Local Similarity 88.7%;
Matches 597; Conservative
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                                              10.7%; Score 337; DB 2; Length 653;
llarity 23.6%; Pred. No. 5.1e-16;
Conservative 77; Mismatches 231; Indels 206;
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Patent No. 6863889
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; ORGANISM: Homo
US-09-520-781-10
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US-09-957-187-10
                                                                              Matches 159;
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; Patent No. 6942992
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard A.
; IITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES ENCODING HUMAN SLIT-,
                                                                                                                                                                                                                                                                                                                                                                                      Gapa
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PRIOR FILING DATE: 2000-09-20

PRIOR APPLICATION NUMBER: 60/233,798

PRIOR FILING DATE: 2000-09-19

PRIOR PILING DATE: 2000-01-04

PRIOR FILING DATE: 2000-01-04

NUMBER OF SEQ ID NOS: 85

SOFTWARE: PATENTIN Ver. 2.1
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Matches 159; Conservative
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TYPE: PRT
ORGANISM: Homo sapiens
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SENERAL INFORMATION:
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SEQ ID NO 12
LENGTH: 590
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TITLE OF INVENTION: MEGF-, AND ROUNDABOUT-LIKE POLYPEPTIDES CURRENT APPLICATION NUMBER: US/09/991,053
CURRENT APPLICATION NUMBER: US/09/991,053
CURRENT FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: USSN 60/123,667
PRIOR APPLICATION NUMBER: 09/520,781
PRIOR FILING DATE: 2000-03-08
NUMBER: OP/520,781
NUMBER: OP/520,781
SEQ ID NOS: 81
SOFTWARE: PAUGHLIN Ver. 2.1
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TYPE: PRT
ORGANISM: Homo sapiens
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US-09-991-053-10
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Sequence 12, Application US/09520781 Patent No. 6689866

RESULT 14 US-09-520-781-12

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APPLICANT: Shimkets, Richard A.
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND PROTEINS ENCODED THEREBY
FILE REPERENCE: 15966-540 No. 6689866el Polynucleotides
CURRENT APPLICATION NUMBER: US/09/520,781
CURRENT FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: USN 60/123,667
PRIOR PILING DATE: 1999-03-09
NUMBER OF SEQ ID NOS: 81
SOFTWARE: Patentin Ver. 2.0
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APPLICANT: LaRochelle, William
TITLE OP INVENTION: NOVEL POLYNUCLEOTIDES AND PROTEINS ENCODED THEREBY
FILE REFERENCE: 15966-540 [OIP
CURRENT APPLICATION NUMBER: US/09/957,187
CURRENT APPLICATION NUMBER: 05/02.19
PRIOR APPLICATION NUMBER: 05/123,667
PRIOR FILING DATE: 1999-03-09
PRIOR PRDIICATION NUMBER: 09/520,781
PRIOR FILING DATE: 2000-03-03
PRIOR PELING DATE: 2000-03-03
PRIOR APPLICATION NUMBER: 60/234,082
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Pred. No. 8.7e-16;
0; Mismatches 187;
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US-09-520-781-12
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Best Local Similarity
Matches 130; Conserv
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Best Local Similarity 25.8%; Pred. No. 8.7e-16;
Matches 130; Conservative 60; Mismatches 187; Indels 126; Gaps
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PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: 60/233,798
PRIOR PILING DATE: 2000-09-19
PRIOR APPLICATION NUMBER: 60/174,485
PRIOR FILING DATE: 2000-01-04
NUMBER OF SEQ ID NOS: 85
SOFTWARE: PatentIN Ver. 2.1
SEQ ID NO 12
LENGTH: 590
TYPE: PRT
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US-09-957-187-12
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R;Titani, K.; Takio, K.; Handa, M.; Ruggeri, Z.M.
Proc. Natl. Acad. Sci. U.S.A. 84, 5610-5614, 1987
A;Title: Amino acid sequence of the von Willebrand factor-binding domain of platelet memt
A;Reference number: A94173; WUID:87289654; PMID:3497398
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A;Cross-references: UNIPARC:UPI000073621; GB:S34436; NID:g249176; PIDN:AAB22152.1; PID:ç
A;Note: variant D
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R;Lopez, J.A.; Ludwig, E.H.; McCarthy, B.J.
R.Biol. Chem. 267, 10055-10061, 1992
A;Title: Polymorphism of human glycoprotein Ib alpha results from a variable number of
                                                                                                                                                                                                                                                          A;Cross-references: UNITARC:UP10000174312
R;Hess, D.; Schaller, J.; Rickli, B.E.; Clemetson, K.J.
Eur. J. Biochem. 199, 389-393, 1991
A;Title: Identification of the disulphide bonds in human platelet glycocalicin.
A;Reference number: $16945; WUID:91301149; PMID:2070794
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A,Status: preliminary; translated from GB/EMBL/DDBJ
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A,Cross-references: GDB:118806; OMIM:231200
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A, Residues: 224-227;262-270;277-282 <HES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S:
Matches 160
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A; Residues: 1-626 <LOP>
A; Cross-references: UNIPROT:P07359; UNIPARC:UPI000012B962; GB:J02940; NID:g183499; PIDN:
A; Cross-references: UNIPROT:P07359; UNIPARC:UPI000012B962; GB:J02940; NID:g183499; PIDN:
B; Widcki, A.N.; Walz, A.; Gerber-Huber, S.N.; Wenger, R.H.; Vornhagen, R.; Clemetson, K.J
Thromb. Haemost. 61, 448-453, 1389
A; Title: Isolation and characterization of human blood platelet mRNA and construction of cloning of a GFIb coding cDNA insert.
A; Reference number: A60435; MUID:90020160; PMID:2799758
A; Molecule type: mRNA
        Cross-references: UNIPROT:P35858; UNIPARC:UPI000000088A; GB:M86826; NID:g184807; PIDN:
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<LRR7>
<LRR8>
<LRR9>
<LRR9>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <LR13>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <LR11>
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                                                                                                                                                                                                                                                                                  <LRR5>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                A, Bxperimental Bource: 11ver
A, Bxperimental Bource: 11ver
A, Note: sequence extracted from NCBI backbone (NCBIP:110171)
F;75-98/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRRI>F;99-122/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRRIPSF;123-146/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRRIPF;147-170/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRRIPF;131-244/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRRIPF;131-242/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRRIPF;243-266/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRRIPF;243-266/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRRIPF;243-266/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRIPF;315-338/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRIPF;315-338/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRIPF;315-338/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRIPF;314-34/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRIPF;318-344/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRIPF;411-434/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRIPF;411-434/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRIPF;411-434/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRIPF;418-549/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRIPF;418-549/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRIPF;418-549/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRIPF;507-529/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRIPF;507-529/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRIPF;418-482/Domain: leu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LRLLAAARNPFNCVCPLSWFG----PWVRESHVTLA 246
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A;Residues: 207-467 <WIC>
A;Cross-references: UNIPARC:UPI0000174311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9.6%;
35.5%;
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Best Local S
Matches 98
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Oy 218 LAAARNPENCYCPLSWFGPWYRESHVTLAS-PEETRCHFP 256	Query Match         8.9%; Score 278.5; DB 2; Length 603;           Best Local Similarity         32.8%; Pred. No. 6.7e-09;           Matches         90; Conservative         48; Mismatches         101; Indels         35; Gaps         10;           Qy         6 PLILPLIL LALGP-GVQGCPSGCQCSQPQTVFCTARQGTT         45           Qy         46 VPRDVPPDTVGLXVPENGITMLDASSFAGLPGLQLLDLSQNQTASLRLPRILL	WESULT 6  THESULT 6  THESULT 6  Sit-1 protein homolog - rat  N'Alternate names: WEGF4 protein  C;Species: Rattus norvegicus (Norway rat)  C;Species: Rattus norvegicus (Norway rat)  C;Species: Rattus norvegicus (Norway rat)  C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004  C;Accession: T42218  R;Nakayama, M; Nakajima, D; Nagase, T; Nomura, N; Seki, N; Ohara, O.  Genomics 51, 27-34, 1998  R;Nakayama, M; Nakajima D; Nagase, T; Nomura, N; Seki, N; Ohara, O.  Genomics 51, 27-34, 1998  R;Nakayama, M; Nakajima D; Nagase, T; Nomura, N; Seki, N; Ohara, O.  Genomics 51, 27-34, 1998  R;Nakayama, M; Nakajima D; Nagase, T; Nomura, N; Seki, N; Ohara, O.  A;Reference number: 214126; MUID:98360089; PMID:9633030  A;Reference number: 214126; MUID:98360089; PMID:9633030  A;Residues: 1-1531 cNakch  C;Genetics: A;Genetics: A
Qy 215 LRLLAAARNPENCVCPLSWFGPWVRES	INLPLLIAPALAAVLLAALAAVGAAYCVRRGRAMAAA 533	Query Match  9.0%; Score 281.5; DB 2; Length 603;  Right Local Similarity 32.4%; Pred. No. 4.5e-09;  Matches 92; Conservative 49; Mismatches 106; Indels 37; Gaps 11;  Qy 6 PLLPLLLL-LALGP-GVQG

Db 125 LSGSRLDEVRAGAPEHLPSLRQLDLSHNPLADLSPFAFSGSNASVSAPSPL 175	Qy 137 FSRLRNLHDLDVSDNQLERVPPVIRGLRGLTRLRLAGATRIAQLRPEDLAGL 188	QY 189 AALQELDVSNLSLQALPGDLSGLFPRLRLIAA 220 :	Qy 221 ARNPENCYCPLSWFGPWYRESHYTLASPBETRCHFPPRNAGRLLLELDYADFGGPA 276	Qy 277 TTTATV 283  Db 351 SLQTSYV 357	RESULT 8 T13953 MGGFS protein - rat N/Alternate names: slit protein homolog C;Species: Rattus norvegicus (Norway rat) C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004 C;Accession: T13953 # Sequence_revision 20-Sep-1999 #text_change 09-Jul-2004	A,Title: Identification of high-molecular-weight proteins with multiple EGF-lik A,Recension: T13953 A,Accession: T13953 A,Status: preliminary; translated from GB/EMBL/DDBJ A,Molecule type: mRNA	A, Residues: 1-1523 <nak> A, Residues: 1-1523 <nak> A, Cross-references: UNIPROT:088280; UNIPARC:UPI00000E5F7A; EMBL:AB011531; NID:93449291; C, Genetics: A, Gene: MEGF5 C, Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein</nak></nak>	Query Match 8.3%; Score 261; DB 2; Length 1523; Best Local Similarity 26.3%; Pred. No. 2e-07; Matches 93; Conservative 41; Mismatches 126; Indels 94; Gaps 14;	Qy 24 CPSGCQCSQPQTVFCTARQGTTVPRDVPEDTVGLYVFENGITMLDASSFAGLFGLLLDL 83	igen Oy	Qy 144 HDLDVSDNQLERVP-PVIRGLRGLTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQ 202	Qy 203 Db 851	QY 263 LLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSLAPTWLSPTAPATEAPSPSTAP 322	Qy 323 PTVGPVPQPQDCPPSTCLNGGTCHLGTRHHLACLCPBGFTGLYCE 367 :::	RESULT 9 B36665 B36665 B1it protein 2 precursor - fruit fly (Drosophila melanogaster) C;Species: Drosophila melanogaster C;Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 02-Aug-2002
Matches 127; Conservative 56; Mismatches 207; Indels 102; Gaps 16;	QY 6 PLILPLILLIALGPGVQGCPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVFENGIT 65	Qy 66 MLDASSFAGLPGLDLSQNQIASLRLPRLLLLDLSHNSLLALEPGIL-DTANVBALRL 124	QY 125 AGLGLOQLDEGLFSRLRNLHDLDVSDNQLERVP-PVIRGLRGLTRLRLAGNTRIAQLRPE 183	OY 184 DLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPFNCVCPLSWFGFWVRESHV 243  Db 176 AFRALRGLEVLTLNNNNITTIPVSSFNHMPKLRTFRLHSNHLFCDCHLAWLSQWLRQ-RP 234	Qy 244 TLASPEETRCHFPPKNAGRILLELDYADFGCPATTTATVPTTRFVVREPTALSSSLAPT 303  235 TIGLFTQCSGPASLRGLNVAEVQKSEFSCSGQCBAAQVPACTLSSGSCPA 284  Qy 304 WLSPTAPATEAPSPPTAPPTVGPVPQPQDCPPSTCLNGGTCHG 348	DD 334 KLRRIDLSNNQIAEIAPDAPQGL	Qy 451 RPNATYSVCVMP 462  Db 429 RAIQTLHLAGNP 440	RESULT 7 A53531 oncofetal trophoblast glycoprotein 5T4 precursor - human	5T4 nn 27-Jun-1994 #text_change 09-Jul-2004	R.Myers, K.A.; RahrSaund, V.; Davtson, M.D.; Young, U.A.; Cheater, A.U.; Stern, F.D. J. Biol. Chem. 269, 9319-9324, 1994 A;Title: Isolation of a cDNA encoding 574 oncofetal trophoblast glycoprotein. An ant A;Reference number: A53531; MUID:94179356; PNID:8132670	NITBABC.IIDIOOOGAGABE. EMBI729083. NID.443	White the control of	Query Match 8.4%; Score 264.5; DB 2; Length 420; Best Local Similarity 28.1%; Pred. No. 2.9e-08; Matches 103; Conservative 44; Mismatches 121; Indels 99; Gaps 15;	Qy 2 CSRVPLLLPLLLLALG	Qy 27 GCQCSQ-PQTVFCTARQGTTVPRDVPDDTVGLYVFENGITMLDASSFAGLPGLQLLD 82

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slit protein 1 precursor - fruit fly (Drosophila melanogaster)
(Species: Drosophila melanogaster
(Species: Jo-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 02-Aug-2002
(SAccession: A36665; A31640; 313523
(Risothberg, J.M.; Jacobs, J.R.; Goodman, C.S.; Artavanis-Tsakonas, S.
(A) A; Title: an extracellular protein necessary for development of midline glia and contaction number: A36665; MUID:91099665; PMID:2176636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 1-1480 <ROT>
A;Cross-references: UNIPARC:UP10000150FD1; GB:X53959; NID:g8614; PIDN:CAA37910.1; PID:g8
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A;Introns: 1381/3
C;Superfamily: fruit fly grottein; EGF homology; leucine-rich alpha-2-glycoprotein r
C;Superfamily: fruit fly protein; EGF homology; leucine-rich alpha-2-glycoprotein r
C;Keywords: alternative splicing; growth factor
C;Keywords: alternative splicing; growth factor
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F;101-124/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;105-1248/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;107-120/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F;107-120/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F;208-272/Domain: proteoglycan carboxyl-terminal homology <PAH2>
F;208-372/Domain: proteoglycan amino-terminal homology <P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Rothberg, J.M.; Hartley, D.A.; Walther, Z.; Artavanis-Tsakonas, S.
1647-155, 1988
A;Title: slit: An EGF-homologous locus of D. melanogaster involved in the development of
A;Reference number: A31640; MUID:89077533; PMID:3144436
                                                                                                QDCPPSTCLNGGTCHLGTRHHLACLCPEG 360
                                                                                                                                                                                      928 REYQC-----LCQPGYHGKHCEFMIDACYGNPCRNNATCTVLEEGRFSCQCAPG 976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ,Molecule type: DNA
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,;Cross-references: UNIPARC:UP1000016BD7A; GB:M23543; NID:g340939; PID:g514357
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ilarity 21.4%; Pred. No. 4e-07;
Conservative 52; Mismatches 168;
                                                                                           TEAPSPPSTAPPTVGPVPQP
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F;1068-1099/Domain: EGF homology
F:1115-1148/Domain: EGF homology
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977 YTGARCETNI 986
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Best Local Similarity
Matches 105; Conserv
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C;Accession: B3665
R;Rothbergy, J. M.; Jacobs, J.R.; Goodman, C.S.; Artavanis-Tsakonas, S.
Genes Dev. 4, 2169-2187, 1990
A;Title: sult: an extracellular protein necessary for development of midline glia and control and con
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : | | : | : | : | | SPEHLINSLITSLINLASNPFNCNCHLAWFAECVRKKSLNGGAARCGAPSKVRDVQIKDLPHS 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         698 EFKCSSENSEGCLGDGYCPPSCTCTGTVVACSRNQLKEIPRGIPAETSELYLESNEIEQI 757
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21.4%; Pred. No. 3.9e-07;
Ive 52; Mismatches 168;
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F;1068-1099/Domain: EGF homology <EGF2>
F;1115-1148/Domain: EGF homology <EGF1>
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Matches 105; Conservative 52;
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CPSGCQCSQPQTVFCTARQGTTVPRDVP	149	RESULT 11 G/G973 synleurin - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 25-Aug-2003 #sequence_revision 25-Aug-2003 #text_change 15-Sep-2003 C;Date: 25-Aug-2003 #sequence_revision 25-Aug-2003 #text_change 15-Sep-2003 C;Date: 25-Aug-2003 #sequence_revision 26: Jan. 8.	Query Match         8.0%;         Score 251;         DB 2;         Length 622;           Best Local Similarity 23.1%;         Pred. No. 2.7e-07;         Additional conservative 52;         Mismatches 142;         Indels 162;         Gaps 13;           Qy         2 CSRVPLLLPLILLALGAGVGCPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVFE 61

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usma protein is not known.

-glycoprotein; leucine-rich alpha-2-glycoprotein repeatin; plasma; tandem repeat
in; plasma; tandem repeat
-g-glycoprotein repeat homology <LRR1>
-g-glycoprotein repeat homology <LRR2>
-g-glycoprotein repeat homology <LRR4>
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-g-glycoprotein repeat homology <LRR5>
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-1910, 1985
Indem repetition of a 24-amino acid segment in the I
241; PMID:3856868
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PVPQLRVLDLTRNALTGLPPGLFQASATLDTLVLKE 114
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                                                                LGLQQLDEGLFSRLRNLHDLDVSDNQLERVPP-VIR 161
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-----EGLFSRLRNLHDLDVSDNQLERVPP-VIR 161
                                                                                                                                                                                                                                                                                                                                                                                                                ---LSGLFPR----LRLLAAARNPFNCVCPLS 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SFNNLTALHPRVLKPLSSLIHLQANSNPWECNCKLL 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PKNAGRLLLELDYADFGCPATTTTATVPTTRPVVRE 292
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PSMRGRALRYINITN----CVTSSINVSRAWAVVKS 420
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. No. 3.4e-07;
ismatches 94; Indels 105; Gaps
                                                                                                                                                                                                     AGLAALOELDVSNLSLQALPGD----
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Qy 199 LSLQALPGDLSGLFPRLRLLAAARNPFNCVCPLSWFGPWVRES 241	
Qy 242 HVTLASPEETRCHFPEKNAGRLLL 265  283 KDKMFSQNDTRCAGPEAVKGQTLL 306	C; Keywords: blocked amino end; glycoprotein; platelet; tandem repeat; transmembrane prot Query Match Best Local Similarity 27.2%; Pred. No. 1e-06; Matches 109; Conservative 28; Mismatches 111; Indels 152; Gaps 14;
RESULT 13 A60164 platelet membrane glycoprotein V precursor - human C;Species: Homo sapiens (man)	Qy 57 LYVFENGITMLDASSFAGLPGLQLLDLSONQIASLRLPRLLLLDLSHNSLLALE 110
C;Date: 12-Jan-1993 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004 C;Accession: A48030; A60164; A35483; B35483; C35483; A60432; A47507; S34329 R;Lanza, F.; Morales, M.; de La Salle, C.; Cazenave, J.P.; Clemetson, K.J.; Shimomura, T J. Biol. Chem. 268, 20801-20807, 1993	Qy 111 PGILDT-ANVEALRIAGLGLQQLDEGLFSRLRNLHD 145
A,Title: Cloning and characterization of the gene encoding the human platelet glycoprote A,Reference number: A48030; MUID:94012616; PMID:8407908 A,Accession: A48030 A,Molecule type: DNA	OY 146 LDVS 162
A.Residues: 1-560 <laz> A.Residues: 1-560 <laz> A.Cross-references: UNIPROT:P40197; UNIPARC:UPI000004B117; EMBL:Z23091; NID:g312501; PID A.Schimomura, T.; Fujimura, K.; Maehama, S.; Takemoto, M.; Oda, K.; Fujimoto, T.; Oyama, Blood 75, 2349-2356, 1990</laz></laz>	Qy 163LRGLTRLRLAGNTRIAQLRPEDLAGLAALQELDV
A,Title: Rapid purification and characterization of human platelet glycoprotein V: the a A,Reference number; A60164; MUID:90275263; PMID:2350580 A,Accession: A60164 A,Accession: A60164 A,Accession: A60164	QY 197SNLSLQALPGDLSGLFPRLRLLAAARNPFNCV 228
A; Residues: 365-384, XX, 386-390, XX, 392-395, XX, 397; 188-208, 11, 210; 27-50, XX, 52-53; 174- , XX, 108, TT; 61-72, TK, 75-77; VV, 56-57; G', 479-487, XX, 489-498, XX, 500, XX, 502-503, XX A; Cross-references: UNIPARC: UDIO001702F8; PPD: INTPARC: INTPARC: INTERPORT: INTE	QY 229 CPLSWFGPWYRESHVTLASPEE-TRCHFPPKNAGRLLLELDYADFGCPATTTATVPTTR 287
R;Roth, G.J.; Church, T.A.; McMullen, B.A.; Williams, S.A. Biochem. Biophys. Res. Commun. 170, 153-161, 1990 A;Title: Human platelet glycoprotein V: a surface leucine-rich glycoprotein related to a A;Reference number. A;Reference number. A;Reference number.	QY         288 PVVRBPTALSSSLAPTWLSPTAPATEAPSPPSTAPPTVGP         327           DD         479 PPRPAADSSSEARVHPALAPNSSEP         503
A,Accession: A35483 A,Molecule type: protein	RESULT 14
A.Residues: 145-166,'I', 168-169,'X',171-172 <rot> A,Cross-references: UNIPARC:UP1000017C303 A,Note: this proteolytic fragment was designated peptide M392 A,Accession: B35483</rot>	JC7763 neuronal leucine-rich repeat protein-3 - rat C.Species: Rattus norvegicus (Norway rat) C.Date: 01-Feb-2002 #sequence revision 01-Feb-2002 #Fext change 09-Jul-2004
A.Molecule type: protein A.Residues: 121-129,'W',131-135,466-468,'X',470 <ro2> A.Cross-references: UNIPARC:UP1000017C304; UNIPARC:UP1000017C305 A.Note: this material was designated peptide M393 but may contain two peptides</ro2>	H. regulation
A.Accession: C35483 A.Molecule type: protein A.Residues: 252-266,1H', 268-272,'X',274-279,'I',281-284,'I',286 <ro3></ro3>	A;Reference number: JC7763; PMID:11549284 A;Contents: Fibrosarcoma cells A;Accession: JC7763
A.T.U.S. Telefiles: UNITARY: UTIONOIT. L.S.O. A.Note: this proteolytic fragment was designated peptide M401 Phramb Des 53, Walz, D.A. 1989	A; Molecule type: mkNA A; Residues: 1-707 < FUK> A; Cross-references: UNIPROT: 09ESY6; UNIPARC: UPI00004F0F2; GB: AF291437
A.Title: Platelet membrane glycoprotein V: characterization of the thrombin-sensitive gl A.Reference number: A60432; MUID:89162331; PMID:2922700 A.Accession: A60432	C:Comment: Ints protein, a new member of the neuronal leucine-rich repeat protein ramily in protein-protein interaction and functions as a cell adhesion molecule or soluble liga. C:Genetics: A:Gene: nlrr-3
A; Molecule type: protein A; Residues: 477-478, FX, 481-485, 'E', 487, 'V', 489-492, 'NQ', 495, 'E', 497-498 <zaf></zaf>	
A:Tross-references: UNIFARC:UP100017C307 R:Hickey, M.J.; Hagen, F.S.; Yagi, M.; Roth, G.J. Proc. Natl. Acad. Sci. U.S.A. 90, 8327-8331, 1993 • A:Title: Human platelet qlycoprotein V: characterization of the polypeptide and the rela	Query Match 7.6%; Score 237; DB 2; Length 707; Best Local Similarity 20.7%; Pred. No. 2e-06; Matches 127; Conservative 80; Mismatches 222; Indels 186; Gaps 22;
	QY 6 PLILPLILLIALGPGVQGCPSGCQCSQPQTVFCTARQGTTVP 47
A.Residues: 1-560 «RES» A.Residues: 1-560 «RES» A.Cross-references: UNIPARC:UPI000004B117; GB:L11238; NID:g388759; PIDN:AAA03069.1; PID: C;Comment: This platelet membrane protein is a substrate for thrombin.	QY 48 RDVPPDTVGLYVFENGITMLDASSFAGLP-GLQLLDLSQNQIASL 91
C;Comment: This protein is absent in Bernard-Soulier syndrome. C;Genetics:	Qy 92RLPRLLLLDLSHNSLLALEPGIL

Db 338EGAFNDLSALSHLAIGANPLYCDCNMQMLSDWVKSEYKEPGIARCAGPG 386  Qy 258 KNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSLAPTWLSPTAPATEAFSP 317    1   1   1	
Db 123 LEENKLTELPEKCLYGLSNLQELYVNHNLLSAISPGAFVGLHNLLRLHLNSNRLQMINSK 182  Qy 115DTAAVVEALRL	RESULT 15  14.26.26  Secreted leucine-rich repeat-containing protein SLIT2 - mouse (fragment)  Nylternate names: neurogenic extractivity slit protein  C;Botte: 11-2na-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004  C;Accession: 174266  R;Alolmes, G. P.; Negue, K.; Burridge, L.; Raman, S.; Algar, E.; Yamada, T.; Little, M.H.  Mech. Dev. 79, 57-72, 1998  A,Tille: Distrinct but overlapping expression patterns of two vertebrate slit homologs in  A,Reference number: 222177; MUID:99279238; PMID:10349621  A,Residues: Perliminary translated from GB/EMBL/DDBJ  A,Residues: The perliminary slit protein; EGF homology; leucine-rich alpha-2-glycoprotein r  A,Residues: Slit2  C;Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein r  Query Match  Best Local Similarity 24.0%; Pred. No. 6.98-06;  Matches 89; Conservative 32; Mismatches 122; Indels 128; Gaps 13;  Cy CPSCCCCSOPOTTECTARGTTVPRDVPPDTVPTVENDITAUDASSPAGLPGIOLDLD 83  ELS CROSSCOLD-TYVRCSNRGIRKUPREDVENDITAUPASSPAGLPGIOLDLD 89  A) SQN 188 RQNOIASLRLPRILLDLESHNRIADLENDITANYBAIRIAGLEQUEDES 137

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                                                                                                    ALRLAGIGLQQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLRGLTRLRLAGNTRIAQL 180
                                                                                                                  SHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSL 300
                                                                                                                                                                                                                                                           APTWLSPTAPATEAPSPPSTAPPTVGPVPQPQDQDCPPSTCLNGGTCHLGTRHHLACLCPEG 360
                                                                                                                                                                                                                                                                         APTWLSPTAPATEAPSPPSTAPPTVGPVPQPQDCPPSTCLNGGTCHLGTRHLACLCPEG 360
                                                                                                                                                                                                                                                                                                             FIGLYCESQMGQGTRPSPTPVTPRPPRSLTLGIEPVSPTSLRVGLQRYLQGSSVQLRSLR 420
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MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
Chen J., Chow B., Chui C., Crowley C., Currell B., Dowd P.,
Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.H.,
Vansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
Wood W.L., Godowski P.J., Gravy A.M.;
"The secreted protein discovery initiative (SPDI), a large-scale
effort to identify novel human secreted and transmembrane proteins: a
              1 MCSRVPLLLPLLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVF
                                                                                                                                                                     Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
MCSRVPLLLPLLLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVF
                                                                                                                                                        RPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPFNCVCPLSWFGPWVRE
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
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Name=SLITL2; ORFNames=UNQ314;
Homo sapiens (Human).
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NEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
A Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Klausner R.D., Collins F.S., Wagner L., Shanmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A popkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Richards S., Worley K.C., Halley M.M., Gadrig A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.W., Sodergren B.J., Lu X., Gibbs R.A.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Kzzywinski M.I., Skalaka U., Smailus D.E.,
Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.
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Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.

REMBL; AY358299; AAQ88666.1; -; mRNA.

REMBL; AX358299; AAQ88666.1; -; mRNA.

RESEMBL; AX5820000168140; HRNA.

RICEPTO; IPRO00742; EGF 2.

INTERPO; IPRO00742; EGF 11ike.

R InterPro; IPRO00510; IEGF.

R InterPro; IPRO01610; IRG.

R InterPro; IPRO01641; IRR.

R InterPro; IPRO01641; IRR.

R InterPro; IPRO01643; IRR. Cterm.

R InterPro; IPRO01843; IRR. Cterm.

INTERPO; IPRO01843; IRR. Cyst.

R InterPro; IPRO01841; IRR. Cyst.
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Pred. No. 1.1e-165;
0; Mismatches 1;
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Pfam; PF00041; fn3; 1.
Pfam; PF00041; fn3; 1.
Pfam; PF00462; LRR\(T); 1.
PRINTS; PR00019; LEURICHRPT.
SMART; SM00181; EGF; 1.
SMART; SM00365; LRR\(T); 8.
SWART; SM00369; LRR\(T); 8.
SWART; SM00369; LRR\(T); 1.
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PROSITE; PS01186; EGF 2; 1.
PROSITE; PS50026; EGF 3; 1.
PROSITE; PS50853; FN3; 1.
SEQUENCE 673 AA; 71655 MW;
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                                                              TRPVVREPTALSSSLAPTWLSPTAPATEAPSPPSTAPPTVGPVPQPQDCPPSTCLNGGTC
                                                                                                                                                                                                                                                        TRPVVREPTALSSSLAPTWLSPTAPATEAPSPPSTAPPTVGPVPQPQDCPPSTCLNGGTC
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Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                         LTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPF
                                                                                                                                    NCVCPLSWFGPWVRESHVTLASPEETRCHPPPKNAGRLLLELDYADFGCPATTTTATVPT
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QGEMK4;
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NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                     75;
                                                                                                                                                                                                                                                                               Query Match 98.2%; Score 3078.5; DB 2; Length 673; Best Local Similarity 88.6%; Pred. No. 2e-165; Matches 596; Conservative 0; Mismatches 2; Indels 75;
                                                                                                                                                                                                                                              891E149652DEA286 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                 ENGITMLDASSFAGLPGLQLLDLSQNQIAS-------
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OBCXI_HUMAN PRELIMINARY; PRT;
Q96CXI;
01-DEC-2001 (TEMBLrel. 19, Created)
PÉAM; PPO1462; LRRCT; 1.
PÉAM; PPO1462; LRRNT; 1.
PÉAM; PPO0560; LRR 1; 6.
PR.NYS; PRO019; LERRICHRPT.
SWART; SM00181; EGF; 1.
SWART; SM00013; LRRCT; 1.
SWART; SM00013; LRRCT; 1.
SWART; SM00165; LRR SD22; 4.
SWART; SM00165; LRR ED22; 4.
PROSITE; PS01186; EGF 1; 1.
PROSITE; PS01186; EGF 2; 1.
PROSITE; PS00026; EGF 2; 1.
PROSITE; PS00026; EGF 2; 1.
PROSITE; PS0003; PS071 1.
PROSITE; PS0003; PS071 1.
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 9 days embryo whole body cDNA, RIKEN full-length enriched
library, clone:D030066D07 product:hypothetical Prokaryotic membrane
lipoprotein lipid attachment site/Cysteine-rich flanking region, N-
terminal/Leucine-rich repeat/EGF-like domain/Leucine-rich repeat,
                                       AQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPFNCVCPLSWFGPW
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
      ------LRLPRILLIDLSHNSLLALEPGILDTA
                                                                                                                                 NVEALRLAGIGLOQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLRGLTRLAGNTRI
                                                                                                                                                                         NVEALRLAGLGLOOLDEGLFSRLRNLHDLDVSDNOLERVPPVIRGLRGLTRLRLAGNTRI
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MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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MEDLINE-21085660; PubMed-11217851; DOI-10.1038/35055500;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
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Altausherg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Butchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
A. Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
Brasa S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Brichards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A. Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.W., Gay L.J., Hulyk S.W.,
A. Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield X.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Broneration and initial analysis of more than 15,000 full-length human
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                      DOI=10.1073/pnas.242603899;
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Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC013767; AAH13767.1; -; mRNA.
HSSP; Q9BZR6; 1PBT.
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   Last sequence update)
Last annotation update)
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Pred. No. 5.4e-144;
); Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                        TISSUE=Lung;
MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000483; LRR_Cterm.
InterPro; IPR003591; LRR_typ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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InterPro; IPR006209; EGF Ilke.
InterPro; IPR003841; FU III.
InterPro; IPR006210; IEGF.
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EGF-like domain; Leucine-rich
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SWART; SM00060; FN3; 1.
SWART; SM00082; LRRCT; 1.
SWART; SM00369; LRR TYP; 2.
PROSITE; PS00122; EGF_1; 1.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS0026; EGF_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00008; EGF; 1.
Pfam; PF000041; fn3; 1.
Pfam; PF01463; LRRCT; 1.
Pfam; PF00560; LRR 1; 6.
PRINTS; PR00019; LEURICHRPT.
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(TrEMBLrel. 19, (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87.4%;
                          01-MAR-2004 (TrEMBLrel. 26
SLITL2 protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001611; LRR.
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nes 525; Conservative
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                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                Name=SLITL2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Lung;
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A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Golobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gasterland T., Gissi C., King B., Kochwa H., Kuchl P., Lewis S., Marsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Barai K., Okido T., Furuno M., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Bronsetein M.J., Bult C., Fletcher C., Fullita M., Gariboldi M., A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H. Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Winnshaw-Bonis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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STRAIN=C57BL/6J; TISSUB=Whole body;

A dadachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,

A dadachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,

Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,

Hayashida K., Hayatsu N., Hiramoto K., Kanoka T., Kasukawa T.,

Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,

Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,

A Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,

Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,

Tagawa A., Takahashi P., Takaku-Akahira S., Takada T.,

Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
STRAIN-ECYBEL/G1; TISSUE=Whole body;
The REANTOM CONSORTIUM.
THE RIKEN GENOME Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-C57BL/6J; TISSUE=Whole body;
MEDLINE=20499374; Pubmed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramateu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length GDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1650(2000).
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Shibata K., Itoh M., Aizawa K., Nagacka S., Sasaki N., Carninci P., Shibata K., Itoh M., Aizawa K., Nagacka S., Sasaki N., Carninci P., Sumi N., Ishii K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii K., Matamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa W., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Rikiki integrated sequence analysis (RISA) system-384-format Sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                                                                     Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
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HSSP; P00740; 1EDM.
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InterPro; IPR000742; EGF 2.
InterPro; IPR006209; EGF like.
InterPro; IPR003611; FN III.
InterPro; IPR006210; IEGF.
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InterPro; IPR001611;
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186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HHLACLCPEGFTGLYCESQMGQGTRPSPTPVTPRPPRSLTLGIEPVSPTSLRVGLQRYLQ 410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   606 TSTAQDKGQVGPGTGPLELEGVKAPLEPGSKATEGGGBALSGGPECEVPLMGYPGPSLQG 665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78;
                                                                                                                                                                                                                                                       79.5%; Score 2491; DB 2; Length 673; 73.5%; Pred. No. 2.6e-132; ive 25; Mismatches 74; Indels 76
                                                                                                                                                                                                                                72284 MW; E35D1B35DDFF5EDB CRC64;
                                                                                                                                                                                                                                                                                                                                                        66 MLDASSFAGLPGLQLLDLSQNQIAS----
                                                                                                                                                       SMART; SM00369; LRR TYP; 3.
PROSITE; PS00022; EGF 1; UNKNOWN 1.
PROSITE; PS00186; EGF 2; 1.
PROSITE; PS50026; EGF 3; 1.
PROSITE; PS50853; PN3; 1.
Hypothetical protein; Lipoprotein.
SEQUENCE 673 AA; 72284 MW; E35D11
                              Pfam; PF00008; EGF; 1.
Pfam; PF00004; ff13; 1.
Pfam; PF00041; ff13; 1.
Pfam; PF00463; LRRCT; 1.
Pfam; PF00560; LRR 1; 6.
PRINTS; PR00019; LEURICHRPT.
SWART; SW00081; EGF; 1.
SWART; SW00082; LRCT; 1.
SWART; SW00082; LRRCT; 1.
SWART; SW00013; LRRUT; 1.
           InterPro; IPR000372; LRR_Nter
InterPro; IPR003591; LRR_typ.
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SIGNAL
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
                                                                                                                                                                                                                                                                                                                                       (Slitl2)
                                                                                                                                                                                                                                                                                                                     Schrewe H., Kutejova E.; "Structure and expression analysis of the mouse Slit-like 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=FVBLN; TISSUE-Kidney;
Director MGC Project;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ458938; CAD30331.1; -; mRNA.
EMBL; BC050274; AAH50274.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                      Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                               01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
21it-like 2 protein precursor.
Name=Slit(12)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Nat1. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                 673 AA
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MGI; MGI:2177651; Slit12.
InterPro; IPR00042; EGF_2.
InterPro; IPR006209; EGF_like.
InterPro; IPR003961; FN_III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; PR001611; IRR.
InterPro; PR001641; IRR. Cterm.
InterPro; PR000483; IRR_Nterm.
InterPro; PR000372; IRR_Typ.
Pfam; PF000089; ISCF; 1.
Pfam; PF01463; IRRCT; 1.
Pfam; PF01463; IRRCT; 1.
Pfam; PF01463; IRRUT; 1.
Pfam; PF01463; IRRUT; 1.
Pfam; PR00560; IRRUT; 1.
SMART; SM00189; IEGNRICHRPT.
SMART; SM00081; IRGF; 1.
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                                              QBR2GS MOUSE PRELIMINARY,
QBR2GS;
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                                                                                                                                                                                                                              Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                             NCBI_TaxID=10090;
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           RESULT GRESULT GRESULT
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306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         187 AGILDTANVEALRLAGLGLRQLDEGLFCRLLINLHDLDVSDNQLEHMPSVIQGLRGLTRLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111 PGILDTANVEALRLAGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLRGLTRLR
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09CZT5,
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 10 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2610528G05 product:hypothetical Prokaryotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tch 79.4%; Score 2490; DB 2; Length 6 al Similarity 73.5%; Pred. No. 3e-132; 491; Conservative 25; Mismatches 74; Indels
                                                                                                                                                                                                                                                                                                                                                                                          1 24 Potential.
25 673 Slit-like 2 protein.
673 AA; 72260 MW; AABBDA82DA8E9D32 CRC64;
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SMART; SM00013; LRRNT; 1.
SMART; SM00369; LRR TYP; 3.
PROSITE; PS00022; EGF 1; UNKNOWN_1.
PROSITE; PS01186; EGF 2; 1.
PROSITE; PS50026; EGF 3; 1.
PROSITE; PS50853; FN3; 1.
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C STRAIN-CSTBL/63; TISSUB-Whole body;

K MEDLINE-2108560; PubMed=11217851; DOI=10.1038/3505500;

K MEDLINE-2108560; PubMed=11217851; DOI=10.1038/3505500;

K MEDLINE-2108560; PubMed=11217851; DOI=10.1038/3505500;

A Arawa J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arawa T., Hara A., Pukunishi Y., Komoo H., Kasukawa T., Santo T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsudi F., Suzuki R., Tomita M., Wagner L., Washio T.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Brownstein M.J., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Nyanshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Nanabalia A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                    STRAIN=C57BL/6J; TISSUE=Whole body;
MBDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
                       region, N-terminal/Leucine-rich repeat/EGF-like domain/Leucine-rich repeat, typical subtype/Leucine-rich repeat, outliers/Cysteine-rich flanking region, C-terminal/Leucine-rich region/Fibronectin type III domain containing protein, full insert sequence.
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  membrane lipoprotein lipid attachment site/Cysteine-rich flanking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=CS7BL/6J; TISSUE=Whole body;
The FANTOM Consortium,
                                                                                                                                                                                                                     Muridae; Murinae; Mus.
                                                                                                                                             musculus (Mouse)
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NUCLEOTIDE SEOUENCE
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                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                   Name=Slitl2;
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186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67 TLDVGCFAGLPGLQLLDLSQNQITSLPGGIFQPLVNLSNLDLTANKLHEISNETFRGLRR 126
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                          Adachi J. Alzawa K., Akahira S., Akimura T., Arai A., Aono H., Adachi J., Alzawa K., Akahira S., Akimura T., Arai A., Aono H., Adachi J., Alzawa T., Bono H., Carninci P., Fukunda S., Fukunishi Y., Furuno M., Hanagaki T., Hara A., Hayatuu N., Hiramoto K., Hiraoka T., Hori F., Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H., Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M., Okazaki Y., Okido T., Owa C., Saito H., Sakai K., Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T., Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T., Miramateu M., Hayashizaki Y., Summura T., Yasunishi A., Yoshino M., Miramateu M., Hayashizaki Y.; Submitted (Jul. 2000)
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25; Mismatches
                                                                                                                                                                                                                                          EMBL; AKO12169; BAB28075.1; -; mRNA.
HSSP; P00740; IEDM.
Ensembl; ENSWMG500000035646; Mus musculus.
MgI; MGI:2177551; Slitl2.
InterPro; IPR000742; EGF 2.
InterPro; IPR00509; EGF 7.
InterPro; IPR0051951; FN III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PRO0019; LEURICHRPT.
SWART; SMOO181; EGF; 1.
SWART; SMOO060; FR3; 1.
SWART; SMOO131; LRRCT; 1.
SWART; SMOO131; LRRWT; 1.
SWART; SMOO131; LRRWT; 1.
PROSITE; PSOO122; EGF 1; UNKNOWN 1.
PROSITE; PSOO186; EGF 2; 1.
PROSITE; PSSOO26; EGF 2; 1.
PROSITE; PSSOO26; EGF 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                          Interpro; 1PR000483; IRR_Cterm.
Interpro; IPR000372; LRR_Nterm.
Interpro; IPR003591; LRR_typ.
Pfam; PP00008; EGF; 1.
Pfam; PP00041; fn3; 1.
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72336 MW; 9C5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PP01463; LRRCT; 1.
Pfam; PP01462; LRRNT; 1.
Pfam; PF00560; LRR 1; 6.
PRINTS; PR00019; LEURICHRPT
                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR006210; IEGF.
InterPro; IPR001611; LRR.
InterPro; IPR000483; LRR_Ct
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SEOUENCE 673 AA; 72
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InterPro, IPR000483; LRR_Cterm.
InterPro, IPR003885; LRR_Cyst.
InterPro, IPR003591; LRR_typ.
                                                                                                                                                                                                                                                                                               Query Match 38.7%;
Best Local Similarity 41.3%;
Matches 282; Conservative 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q503G2_BRARE PRELIMINARY;
Q503G2;
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                                                                                                                                                                                                                                                              SEQUENCE
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WEDLINE=22388257; Pubbled=12477912; DOI=10.1073/pnas.242603899;

X RIAUSBER R.D., Felngold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

A Roperson M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

A Hilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffaud G.G.,

Rhitting M., Madan A., Young A.C., Shevchenko Y., Bouffaud G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Wrzywinski M.I., Shalska U., Smailus D.E.,

Butterfield Y.S.N., Wrzywinski M.I., Shalska U., Smailus D.E.,

Butterfield Y
                                                                                               HHWECLCPEGFIGLYCESPVEQGMKPSSIPDTPRPPDLLPLSIEPVSPTSLRVKLORYLO 486
                                                                                                                                                   GSSVQLRSLRLTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCVMPLGPGRVPE 470
                                                                                                                                                                     GEEACGEAHTPPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRRGRAM 530
                                                                                                                                                                                                                                                  531 AAAAQDKGQVGPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGPGLQS 590
                                                                                                                                                                                                                                                                                                                        HHLACLCPEGFTGLYCESQMGQGTRPSPTPVTPRPPRSLTLGIEPVSPTSLRVGLQRYLQ 410
   REPTALSSSLAPTWLSPTAPATEAPSPPSTAPPTVGPVPQPQDCPPSTCLNGGTCHLGTR 350
                       Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Whole body;
Klein S., Gerhard D.S.;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BCOT6888; AAH76888.1; -; mRNA.
InterPro; IPR000742; EGF 2.
InterPro; IPR006210; EGF like.
InterPro; IPR006210; IEGF.
InterPro; IPR001611; IRR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           661 AA.
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NCBI_TaxID=8364;
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QGDF55;
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Name=MGC88956;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REPTALSSSLAPTWLSPTAP---ATEAPSPPSTAPPTVGPVPQPQD-------CP 335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | :| : || | | | | | : || AGILLS-AAVAAAACYARRR-----KGKGKHSVEDGGPLEMDGVK-----KGLDGKGE
                                                                                                                                                                                                                                                                                                                                                           8 LLPLLLLLALGPGV--QGCPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVFENGIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----STTTGP----PTTTKHLQTBAPTTASTTTTTIPHQEQEEDTQPPQFDFEDTLCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PSTCLNGGTCHLGTRHHLACLCPEGFTGLYCESOMGQGTRPSPTPVTPRPPRSL---TLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               409 POTCLNGGSCHLDPTGQLECECPPGPQGTYCET-----GPVTPAVVTEMYIEQVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       393 IEPVSPTSLRVGLQRYLQGSSVQLRSLRLTYRNLSGPDKRLVTLRLPASLAEYTVTQLRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    453 NATYSVCVMPLGPGRVPEGEEACGEAHT --- PPAVHSNHAP - VTQAREGNLPLLIAPALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     509 AVLLAALAAVGAAYCVRRGRAMAAAAQDKGQVGPGAGPLELEGVKVPLEPGPKATEGGGE
                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                    155;
                                                                                                                                                                                                                                                                            Length 661;
                                                                                                                                                                                                                                                                            38.7%; Score 1213.5; DB 2; Length 41.3%; Pred. No. 2.6e-60; ive 88; Mismatches 158; Indels
                                                                                                                                                                                                                                   71957 MW; AOAC47946BE8DBEA CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              66 MLDASSFAGLPGLQLLDLSQNQIASL----
PÉANT, PEOLOGO BERT LAKE CYP.
PÉANT, PFO1463; LRRCT; 1.
PÉANT, PFO1463; LRRCT; 1.
PRANTS, PRO0019; LEURICHRPT.
SWART; SW00181; EGF; 1.
SWART; SW00362; LRRCT; 1.
SWART; SW00362; LRR SD22; 4.
SWART; SW00369; LRR SD22; 4.
PROSITE; PS01186; EGF 1; 1.
PROSITE; PS01186; EGF 2; 1.
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                                                                                                                                                                                                Greatusberges Sequence.

(STRAINS-SINGADOUR LOCAL Strain; TISSUB-Embryo;

(MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

(MEDLINE=22388257; PubMed=12., Magner L., Schaefer G.D., Raha R.F., Jordan H., Moore T., Max S.I., Wandin G., Haleh F., Marchards M., Marchards M., Poters G.J., Abramson R.D., Mullahy S.J., Malex S.A., McEwan P.J., McKernan K.J., Malex J.A., Guarathe P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Myllalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Macha M., Young A.C., Shevchenko Y., Boulfard G.G., Rahiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G., Rahiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G., Rahiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G., Rahiting M., Macha M., Karywinski M.I., Skalaka U., Smailus D.E., Machin J.E., Jones S.J.M., Marra M.A.;

(Medliyer A.C., Grimwood J., Schmutz J., Marra M.A.;

(Medliyer A.C., Grimwood J., Schmutz J., Marra M.A.;

(Medliyer A.C., Schein J.E., Jones S.J.M., Marra M.A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LYLYSNIIQNIHPAAFEGLENLLELKLQGNQISVLPALQLPRLLHLDLSYNSIPPLVAQD 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LDTANVEALRIAGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLRGLTRLRLAG 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TALSSSLAPTWLSPTAPATEAPSPPSTAPP----TVGPVPQPQD-----CPPSTCLNG 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TNSSTQSGTTH1VPPAPLSDISSADADNFPVYQTTAFPSRIMEDSEGEGIMCPPNICLNG 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTCHLGTRHHLACLCPEGFTGLYCESQMGQGTRPSPTP-----VTPRPPRSLTLGIEP 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 396 VSPTSLRVGLQRYLQGSSVQLRSLRLTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNAT 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPFNCVCPLSW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 643;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29.6%; Score 927.5; DB 2; Length 41.0%; Pred. No. 3.3e-44; ive 75; Mismatches 198; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; BC095341; AAH95341.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (1 protein.
643 AA; 70200 MW; 964BE87924A7C642 CRC64;
13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Hypothetical protein zgc:110624.
Name-zgc:110624;
Brachydanio_rerio (Zebrafish) (Danio_rerio).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                                                                                                                                                                         NUCLEOTIDE SEQUENCE
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                                                                                                                                                     NCBI TaxID=7955;
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YSVCVMPLGPGRVPEGEEACGEAHT---PPAVHSNHAPVTQAREGNLPLLIAPALAAVLL 512
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    172 AGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPFNCVCPL 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWFGPWVRESHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTTATVPTTRPVVR 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Maucell E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A., Maucell E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A., Micallon G., Jaffe D., Fisher S., Luffalla G., Dossat C., Segurens B., Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S., Anthouard V., Jubin C., Castellia V., Katinka M., Vacherie B., Biemont C., Skalliz Z., Cattolico L., Poulain J., De Berardinis V., Cruand C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J., Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S., Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J., Lander D., Cholmson-Rechavi M., Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C., Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.; Genome duplication in the teleost fish Tetraodon nigroviridis reveals
                                                                                                            ||| : || || | | |||||||| AGNP-LGDLRVEDFEKLTSLQELDLSGLNLQGFSPSFLEMFPRLTQLTAAENPFNCLCPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57 LYVFENGITMLDASSFAGLPGLQLLDLSQNQIA---SLRLPRLLLLDLSHNSLLALEPGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              114 LDTANVEALRLAGLGLOGLDEGLFSRLRNLHDLDVSDNQLERVPPVIR--GLRGLTRLRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29.2%; Score 914.5; DB 2; Length 962;
38.0%; Pred. No. 2.8e-43;
iive 77; Mismatches 190; Indels 95; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tetraodon nigroviridis (Gréen puffer).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                    561
                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
Genoscope; Whitehead Institute Centre for Genome Research;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
preliminary data.
                                                                                                                                                                                                 513 AALAAVGAAYCVRRGRAMAAAAQDKGQVGPGAGPLELEGVKVPLEPG---PK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; CAAE01014535; CAF97214.1; -; Genomic DNA.
SEQUENCE 962 AA; 106856 MW; 3EC2C9402AG80BF6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome 19 SCAF14535, whole genome shotgun sequence.
ORFNAMMES=GSTENG00014497001;
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Nature 431:946-957(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-SEP-2005 (TrEMBLrel. 31,
                                                                                                                                                                                                                                                                                                                                                                                                                          Q4SQ68_TETNG PRELIMINARY;
Q4SQ68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=99883;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         222;
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Matches
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TISSUE=EPA, and Lung;

MEDLINE=22388257; PubMed=12477922; DOI=10.1073/pnas.242603899;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Klausner R.D., Collins F.S., Wagner L. H., Derge J.G.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Habieh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

A Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Parange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D. Mullahy S.J.,

A Robas S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S.A., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

A Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,
                       350 RHHLACLCPEGF-----TGLY-CESQMGQG-----TRPSP-TPVTPRP 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         446 TVTQLRPNATYSVCVMPLGPGRVPEGEEACGEAHTPPAVHSNHAPVTQAREGNLPLLIAP 505
                                                                                                                                                                                   ----LLEDQALAGLSSLALLDLSRNQLGTISREALQPLASLQVLRLTENPWRCDCALHW 214
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                                                                                                                                                                                                                                                                                                                                                                                                             318 GCHSASDTGSCMLFLSNITLAHAGKYECEASNAGGAARVPFRLLVNASRQQPQQPAQPPP 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q6PJG9; Q9BWJ0;
10-WAY-2005 (Rel. 47, Created)
10-WAY-2005 (Rel. 47, Last sequence update)
10-WAY-2005 (Rel. 47, Last annotation update)
Leucine-rich repeat and fibronectin type-III domain containing protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                         114 LDTANVEALRLAGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLRGLTRLRLAG
                                                                                                                                                                                                                                                                                                 EPTALSSSLAPTWLSPTAPATEAPSPPSTAPPTVGPVPQPQDCPP--STCLNGGTCHLGT
                                                                                                                                                                                                                                                                                                                                    265 OPLELTANLGED-LRVACQASGYPOP----LVTWRKVPOPREGRPRAQAQLEGGL--LGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                  386 PRSLTLGIEPVSPTSLRVGLQRYLQGSSVQLRSLRLTYRNLSGPDKRLVTLRLPASLAEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----AIAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 506 ALAAVIJLAALAAVGAAYCVRRGRAMAAAAQDKGQVGPGA-----GP---LELEGVK-
                                                                                                                                                174 NTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPFNCVCPLSW
                                                                                                                                                                                                                        234 FGPWVRESHVTLASPEETR - CHPPPKNAGRLLLELDYADFGCPATTTTATVPTTRPVVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          554 -----VPLEPGPKATEGGGEALPSGSECEVPLMGFPGPGLQSP 591
                                                                                                  465 ERGHEMFVINRSKPLFAEGPAEA---PADCG-PAQG-AGPGLRVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----RPEAG-SMAFRALG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       378 PAARPAGSEP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 precursor.
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                                                                                            | SHICPANICLNGGTCHFDPMGQLSCICLSGTSGLYCEN-----VDIVPDPPKHPV 728
                                                                                                                                                                       ---CPPSTCLNGGTCHLGTRHHLACLCPEGFTGLYCESQMGQGTRPSPTPVTPRPPR--- 387
                                                                                                                                                  ---SLTLGIEP-----VSPTSLRVGLQRYLQGSSVQLRSLRLTYRNLSGPDKRLV 434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=LRRC24;
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                         SPTGSTPSIPVSTTPPKMTYTNAIPPPPPPPPSEEILPSKTPYPLPPBPTFSPSSTSGEVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MALRAPALLPLILL-LPLRAAGCPAACRC-YSATVECGALRLRVVPLGIPPGTQTLFLQ
                                                                                                                                                                                                                                             481 PPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYÇVRRGRAMAAAQDKGQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MCSRVPLLLPLLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shimizu N., Asakawa S., Shimizu A., Yamazaki S., Ishikawa S.K.;
"Novel gene contraining Leucine rich repeat on human chromosome 8
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AB178281; BAD97811.1; -; mRNA.
InterPro; IPR00110; Ig-1ike.
InterPro; IPR00110; Ig-1ike.
InterPro; IPR00110; Ig-1ike.
InterPro; IPR00110; Ig-1ike.
InterPro; IPR00189; Ig-2.
InterPro; IPR00189; Ig-2.
InterPro; IPR00189; IRR.Cterm.
InterPro; IPR000189; IRR.Cterm.
InterPro; IPR000189; IRR.Cterm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 195;
                                                                                                                                                                                                                          TLRLPASLAEYTVTQLRPNATYSVCVMPLGP-----GRVPEGEEACGEAHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 513;
                                                                                                                                                                                                                                                                                                                                                                                                PADSDPMELDGMKLGLENGANGT-----LPHKQAQINRCHTPL 936
   EPTALSSSLAPTWLSPTAPATEAPSPPSTAP-----PTVGPVPQPQD-
                                                                                                                                                                                                                                                                                                                                                                          GPGAGPLELEGVKVPLEPGPKATEGGGEALPSG----SECEVPL 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin domain; Leucine-rich repeat; Repeat.
SEQUENCE 513 AA; 55199 MW; 3770FA80D979C1DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.8%; Score 368.5; DB 2; 26.4%; Pred. No. 8.5e-13; ive 63; Mismatches 217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PRO0019; LEURICHRPT.
SMART; SM00409; IG; 1.
SMART; SM00369; IGc2; 1.
SMART; SM00369; LRR TYP; 6.
SMART; SM00082; LRR TYP; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-SEP-2005 (TrEMBLrel. 31,
13-SEP-2005 (TrEMBLrel. 31,
13-SEP-2005 (TrEMBLrel. 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 26.4%
Matches 170; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00560; LRR 1; 5
Pfam; PF01463; LRRCT; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LRRC24 protein.
                                                                                                              619
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349 317

65 TMLDASSFAGLPGLQLLDLSQNQIASL-----RLPRLLLLDLSHNSLLALEPGIL-DTA 117

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Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnarch A., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Potential.
Leucine-rich repeat and fibronectin type-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glycoprotein; Immunoglobulin domain; Leucine-rich repeat; Repeat; Signal; Transmembrane.
SIGNAL
CHAIN
                                                                         and mouse cDNA sequences.",

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

1- 'SUBCELLULAR LOCATION: Type I membrane procein (Potential).

-!- SIMILARITY: Contains I fibronectin type-III domain.

-!- SIMILARITY: Contains I Ig-like (immunoglobulin-like) domain.

-!- SIMILARITY: Contains 7 LRR (leucine-rich) repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Potential).
(Potential).
(Potential).
(Potential).
(Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         III domain containing protein
Extracellular (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cytoplasmic (Potential).
LRR 1.
LRR 2.
LRR 3.
LRR 4.
LRR 5.
LRR 6.
LRR 7.
LRR 7.
LR 10-liked (GlCNAc. ...) (P.
N-linked (GlCNAc. ...) (P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / similarity.
13E6645A17A92EE CRC64;
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27.6%; Pred. No. 3.4e-12;
                                                                                                                                                                                                                                                                                                          Ensembl; ENSG0000173621; Homo sapiens. HGNC; HGNC: 28456; LERN4.
InterPro; IPR003961; FN_III.
InterPro; IPR003599; IG-11ke.
InterPro; IPR007110; IG-11ke.
InterPro; IPR003598; IG-11ke.
InterPro; IPR003598; IG-12ke.
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                                                                                                                                                                                                                                                                             EMBL; BC000207; AAH00207.2; -; mRNA.
EMBL; BC015581; AAH15581.2; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000483; LRR_Cterm.
InterPro; IRR003591; LRR_typ.
Pfam; PF00041; fn3; 1.
Pfam; PF00560; LRR_1; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEAM; PF00560; LRR 1; 6.
PRINTS; PR00019; LEURICHRPT.
SWART; SM0060; FN3; 1.
SWART; SM00409; IG; 1.
SWART; SM00409; IGc2; 1.
SWART; SM00082; LRR TYP; 6.
SWART; SM00082; LRR TYP; 6.
PROSITE; PS50853; FN3; 1.
PROSITE; PS50835; IG_LIKE; 1.
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635 AA;
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Best Local Simi.
Matches 169;
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RIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLR------LLAAARNPFN 226
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                                                                                                                                                                                                                        CVCPLSWFGPWVRESHVTLASPEETR-CHFPPKNAGRLLLELDYADFGCPATTTTATVPT 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPRSL----TLGIEP---VSPTSLRVGLQRYLQGSSVQ-LRSLRLTYRNLSGPDKRLVTL 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            393 ARTAAEGEGTLESEPAVQVTEVTATSGLVSWGPGRPADPVWMFQIQYN--SSEDETLIYR 450
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                                                                                                                                                                                                                                                                                                                                                   -----EPPLIARHTORLWVLEGORATLRCRALGDPAPTMHWVGPDDRLVGNSSRARAFP 332
                                                                                                                                                                                                                                                                                                                                                                                                384
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STRAIN=CSTBL/6G; TISSUE-Head;
A OKAZAKI Y. FULUD M., Kasukawa T., Adachi J., Bono H., Kondo S.,
A OKAZAKI Y., FULUD M., Kasukawa T., Adachi J., Bono H., Kondo S.,
A Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
A Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
Schriml L.M., Kanapin A., Mateuda H., Batalov S., Beisel K.W.,
Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
A Balla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
A Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
A Krani A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
A Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
A Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LRENA MOUSE STANDARD; PRT; 636 AA.
080XUB; Q8K3C4;
10-MAY-2005 (Rel. 47, Last sequence update)
10-MAY-2005 (Rel. 47, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Leucine-rich repeat and fibronectin type-III domain containing protein
                                                                        181 -IDALPPGAFAQLGQLSRLDUTSNRLATLAPD--PLFSRGRDAEASPAPLVLSFSGNPLH
  OALGPPDFRNMTGLVDLTLSRNAITRIGARAFGDLESLRSLHLDGNRLVELGTGSLRGPV
                                                                                                                                                                                                                                                                CNCELLWIR-----RLARPDDLETCASPPGLAGRYFWAVPEGEFSC------
                                                                                                                                                                                                                                                                                                           286 TRPVVREPTALSSSLAPTWLSPTAPAT---EAPSPPSTAPPTVGPVPQ-----PQDCPP
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                                                 NVEALRLAGLGQCLDEGLFSR-LRNLHDLDVSDNQLERVP-PVIRGLRGLTRLRLAGNT
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
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23; 64 9

Gaps

61; Mismatches 281; Indels 101;

Conservative

Similarity

LLPLLLLLLLALGPGVQGCPSGCQC---SQPQTVFCTARQGTTVPRDVPPDTVGLYVFENGI

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A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Klausher R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Lischul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Heng L.,

B Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Diatchenko L., Warusina K., Farmer A.A., Rubin G.M., Hong L.,

B Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Connetein M.J., Uddin T.B., Toshiyuki S., Carninfor P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

B Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

B Chierch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human
Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
Sandelin A., Schneider C., Semple C.A., Sectou M., Shinada K.,
Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
Nerardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang I., Yang I.,
Hirozane-Kishikawa T., Konno H., Nakamura M., Zakazume N., Sakazume N., Sakarume N., Sakazume N., Mayazaki A., Sakai K., Saski D., Shibata K., Shinagawa A.,
Nasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
Birney E., Hayashizaki Y.;
"Analysis of the mouse transcriptome based on functional annotation of Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This Swiss-Prot entry is copyright. It is produced through a collaboration
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III domain containing protein 4.
Extracellular (Potential).
Potential.
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PROSITE; PS50855; FN3; 1.
PROSITE; PS50815; IG LIKE; 1.
Glycoprotein; Immunoglobulin domain; Leucine-rich repeat; Repeat; Signal; Transmembrane.
Signal; Transmembrane.
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-!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
-!- SIMILARITY: Contains I fibrenectin type-III domain.
-!- SIMILARITY: Contains I g-like (immunoglobulin-like) domain.
-!- SIMILARITY: Contains I Ig-like (immunoglobulin-like) domain.
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Ensembl; ENSWOYSEO1200000045045; Mus musculus.
MGI; MGI:2385612; Lrfn4.
InterPro; IPR007110; IG-like.
InterPro; IPR001611; LRR.
InterPro; IPR001611; LRR.
Pfam; PF00041; fn3; 1.
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EMBL; BC023036; AAH23036.1; -; mRNA.
EMBL; BC023156; AAH23156.1; -; mRNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NVEALRIAGLGIQQLDEGLFSR-LRNLHDLDVSDNQLBRVP-PVIRGLRGLTRLAGNT 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 NLQHLILSGNQLGRIAPGAFDDFLDSLEDLDVSYNNLRQVPWAGIGSMPALHTLNLDHNL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 -IDALPPGVFAQLSQLSRLDLTSNRLATLAPD--PLFSRGRDAEASPSPLVLSFSGNPLH 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRPVVREPTALSSSLAPTWLSPTAPAT --- EAPSPPSTAPPTVGPVPQPQD ----- 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----EPPLIARHTQRLWVLEGQRATLRCRALGDPVPTMHWVG----PDDRLVGNSSRA 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLR------LLAAARNPFN 226
                                                                                                                                                                                                                                                                                                                                                                                      433 LVTLRLPASLAEYTVTQLRPNATYSVCVMPLGPGRVPEGEEA-----CGEAHTPPAVHSN
                                                                                                                                                                                                                                                                                                                                                                   8 LLPLLLLLLALGPGVQGCPSGCQC---SQPQTVFCTARQGTTVPRDVPPDTVGLYVFENGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CVCPLSWFGPWVRESHVTLASPEETR-CHFPPKNAGRLLLELDYADFGCPATTTTATVPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  334 -CPPSTCLNGGTCHLGTRHHLACLC--PEGFTGLYCESQM-------GQGTRPSPTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              129 WAFPNGTLEIGVTGAGDAGAYTCIATNPAGEATARVELRVLALPHGGNTSAEGGRPGPSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             381 VTPRPPRSL----TLGIEP---VSPTSLRVGLQRYLQGSSVQ-LRSLRLTYRNLSGPDKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : : | | | | |: 389 IAASARTAAEGEGTLESEPAVQVTEVTATSGLVSWGLGRPADPVWMFQIQYN--SSEDET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CNCELLWIR------RLARPDDLETCASPPTLAGRYFWAVPEGEFSC-------
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                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                    (Potential). (Potential). (Potential). (Potential).
                                                                                                                                                                                                                                                                                                       11.2%; Score 351; DB 1; Length 636; 27.2%; Pred. No. 1e-11; tive 62; Mismatches 276; Indels 116;
                                                                                                                                                       (Potential)
                                                                                                                                                                                                                               .) (Potential)
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                                                                                                                                                    N-linked (GlcNAc...) (
Sy similarity.
    Cytoplasmic (Potential).
                                                                                                                                        Fibronectin type-III
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                                                             LRR 4.
LRR 5.
LRR 6.
LRR 7.
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QBBLUO MOUSE PRELIMINARY;
QBBLUO;
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   Similarity
                                                                                                                                                                                                                                                                           636 AA;
   540
466
467
467
407
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503
TOPO DOM
REPEAT
REPEAT
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DOMAIN
CARBOHYD
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CARBOHYD
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CARBOHYD
DISULFID
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ID OB
AC OB
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STRAIN=CSTBL/64; TISSUB=Aorta and vein;

NEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;

A Radai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arakawa T., Hara A., Pukunishi Y., Konno H., Adachi J., Fukuda S.,

A Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Rieschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

Ruchil P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carminci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fuljita M., Gariboldi M.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakameto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Nurshiaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=CS7BL/6J; TISSUE=Aorta and vein;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
Thalysis of the mouse transcriptome based on functional annotation of
60,770 full-length oDNAs.";
Nature 420:563-573(2002).
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Mus musculus adult male aorta and vein cDNA, RIKEN full-length
enriched library, clone: A530098L04 product:KIAA0405 (LEUCINE-RICH
REPEAT TRANSMEMBRANE PROTEIN FLRT2) homolog (Fibronectin leucine rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=C57BL/63; TISSUE-Aorta and vein;
MEDLINB=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatau N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                      Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=C57BL/6J; TISSUE=Aorta and vein;
MEDLINE-99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
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MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Naihi K., Harama T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; "RIKEN integrated sequence analysis (RISA) system-384-format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                     Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                         transmembrane protein 2).
Name=Map4k5; Synonyms=Flrt2;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 409:685-690(2001).
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NUCLEOTIDE SEQUENCE.
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TISSUE-Mammary tumor. Metallothionien-TGF alpha model. 10 month old virgin mouse. Taken by biopsy;

KEDLINE-2238257; PubMed-1247932; DOI=10.1073/pnas.242603899;

KEDLINE-2338257; PubMed-1247932; DOI=10.1073/pnas.242603899;

RA Straubberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schnefer C.F., Bhat N.K.,

RIGCHIS R.F., Jordan H., Moore T., Max S.I., Wang J., Hsich F.,

A plachul R.F., Jordan H., Moore T., Max S.I., Wang J., Hsich F.,

Rapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Rapleton M., Soares M.B., Rohityki S., Carrinci P., Frange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raba S.S., McEwan P.J., McKernan K.J., Malk J.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garchards P.H., Glabbs R.A., Glabbs R.A.,

Richards S., Worley K.C., Hale S., Garchenko Y., Boulfard G.G.,

Rah, Helton B.K., Muzny D.M., Sodergren E.J., Lu X., Glbbs R.A.,

Rahey J., Helton B.K., Ketreman M., Madan A., Rodrigues S., Sanchez A.,

Rah, Mhiting M., Madan A., Young A.C., Shewchenko Y., Boulfard G.G.,

Ratiguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;

"And moving Chan and initial analysis of more than 15,000 full-length human and moving companienced m.
                                                                                                                                                                                                        Adachi J., Alzawa K., Akimura T., Hara A., Hashizume W., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayatanida K., Hayatan W., Hirokane W., Hayatahida K., Hayatan V., Hirokane T., Hori F., Imotani K., Ishii Y., Itoh M., Kagawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Murata M., Nakamura M., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibate K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., Toya T., Yoya T., Yawunishi A., Muramatsu M., Hayashizaki Y., Tomaru A., Toya T., Yawunishi A., Muramatsu M., Hayashizaki Y.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Mammary tumor. Metallothionien-TGF alpha model. 10 month old virgin mouse. Taken by biopsy.;
NIH MGC Project;
sequencing pipeline with 384 multicapillary sequencer.";
Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=CS7BL/6xCBA;
Haines B.P., Summerbell D., Rigby P.W.J.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases. EMBL; AK04111; BAC30900.1; -; mRNA. EMBL; AY495669; AAR92202.1; -; mRNA. EMBL; BC096471; AAH96471.1; -; mRNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P07359; 1M0Z.
Ensembl; ENSMUSG0000047414; Mus musculus.
MGI; MGI:1925503; Map4k5.
GO:0016021; C:integral to membrane; IEA.
InterPro; IPR003961; FN III.
                                                                                                                               NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/6J; TISSUE=Aorta and vein;
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InterPro; IPR000312; LRR Nterm.
InterPro; IPR0013591; LRR-Lyp.
InterPro; IPR001211; PhospholipaseA2.
Pfam; PP00560; LRR 1, 8.
Pfam; PP01463; LRR 1; 1.
Pfam; PP01463; LRR 1; 1.
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19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       341 NGGTCHLGTRHHLACLCPEGFTGLYCESQMGQGTRPSPTPVTPRPPRSLTLGIEPVSPTS 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | :: | | : | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73 AGLPGLQLLDLSQNQIASLRLP-----RLLLLDLSHNSLLALEPGI---LDTANVEA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             190 NRIAVISDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLTKLKEFSIVRNSLSHPPPDL 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             161 RGLRGLTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAA 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        367 LPVPTPAP-----STVSPTTQSPTL----SVPSPSRGSVPPAPTPSKLPTPDW 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DG----RERVIPPISERIQLSIHFVNDTS 436
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Mus musculus 0 day neonate cerebellum cDNA, RikEN full-length enriched
library, clone:C23002NN12 product:hypothetical Zinc carboxypeptidases,
carboxypeptidase A metalloprotease (Mu4) family containing protein,
full insert sequence (Mus musculus adult male olfactory brain cDNA,
RIKEN full-length enriched library, clone:6430402H13
product:hypothetical Zinc carboxypeptidases A
metalloprotease (M14) family containing protein, full insert
                                                                                                                                                                                                                                                                                                                      4 RVPLLLPLLLLLLLALGPGVQ-----GCPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLY
                                                                                                                                                                                                                                                                                                                                                 11 RGAFILKFWLIISLGLYLQVSKLLACPSVCRCDR-NFVYCNERSLTSVPLGIPEGVTVLY
                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                      85; Mismatches 238; Indels 154;
                                                                                                                                                                                                                   10.9%; Score 341; DB 2; Length 660; 23.1%; Pred. No. 3.9e-11;
                                                                                          PROSITE; PS50853; FN3; 1.
PROSITE; PS0119; PA2 ASP; UNKNOWN 1.
Leucine-rich repeat; Repeat; Transmembrane.
SEQUENCE 660 AA; 73948 MW; 5C1A9BBA3142C020 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           521 AA
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SMART; SM00060; FN3; 1.
SMART; SM00369; LRR TYP; 1.
SMART; SM00082; LRRCT; 1.
SMART; SM00013; LRRNT; 1.
                                                                                                                                                                                                                                                                      Matches 143; Conservative
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QBBHAL;
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60 TQTLFLQDNSIAHLEQGSLAPLAALRHLYLHNYTLRALESGAFRAQPRLLELALTGNRLR 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           268 PSVNV--EPPEFTANLGED-LQVACQASGYPQP----LVVWRKVPQPRDGKPQAQAQLEG 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           436
                                                                                                                                                                                        54 TVGLYVPENGITMLDASSFAGLPGLQLLDLSQNQIASLR-----LPRLLLLDLSHNSLL 107
                                                                                                                                                                                                                                                                                      108 ALEPG-ILDTANVEALRLAGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLRGL 166
                                                                                                                                                                                                                                                                                                                                                                                                                                  -----LLEDQALAGLSSLALLDLSRNQLGTISKEALQPLSSLQVLRLTENPWR 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDCALHWLGSWIKEGGRRLLSSRDKKITCAEPPRLALQSLLEVSGGSLIC-----IP 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTRPVVREPTALSSSLAPTWLSPTAPATEAPSPPSTAPPTVGPVPQPQDCPP--STCLNG 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              343. GTCHLG------TRHHLACLCPEGFTGLY-CESQMGQGTRPSPTPVTPRPPR 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           321 GAPGLGGHGTRDTGSGMLFLTNITLA-----HAGKYECEAANAGGKARVPFHLLVNASR 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----RLPASLAEYT------VTQLRPNATYSVCVM----PLGPGRVPE 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    435 RRRRRRKKVPAPSGEGTLFVNDYSDGPCTFAQLEELRDDHGHEMFVIDRSKPLFPEVLP- 493
                                                                                                                                             59
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                                                                                              1 MCSRVPLLLPL---LLLLLALGPGV----QGCPSGCQCSQPQTVFCTARQGTTVPRDVPPD
                                                                                                                                        MALRAPTLILILILILILIPLIPERPRATGCPAACRC-YSATVECGALRLRVVPPGIPPG
                                                                                                                                                                                                                                                                                                                  120 GLRGGAFVGLVQLRVLYLAGNQLAKLLDFTFLHLPRLQELHLQENSIE-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 227 CVCPLSWFGPWVRESHVTLASPEETR--CHFPPKNAGRLLLELDYADFGCPATTTTATVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           388 SLTLGI-EPVSPTSLRVGLQRYLQGSSVQLRSLRLTYRNLSGPDKRLVTL-----
10.8%; Score 339; DB 2; Length 521; 27.0%; Pred. No. 4e-11;
                                               Indels
                                               66; Mismatches 217;
                      Best Local Similarity 27.08
Matches 149; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GEEACGEAHTPP 482
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Best Local Similarity
RESULT 7
ID ABU80790 standard; p:
DE Human PRO polypeptid
PN US2003036435-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC
                                                                                                                                                                                                          Query Match
Best Local Similarity
RESULT 8
                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
RESULT 9
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                                                                         Query Match
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1: geneseqp1980s:*
2: geneseqp200s:*
3: geneseqp200s:*
5: geneseqp200s:*
6: geneseqp2003s:*
7: geneseqp2003s:*
8: geneseqp2003s:*
8: geneseqp2004s:*
9: geneseqp2004s:*
and is derived by analysis of the total score distribution.

SUMWARIES

Description
GenCore version 5.1.6
- protein search, using sw model
January 5, 2006, 13:52:44; search time 190 Seconds
(without alignments)
1382.887 Million cell updates/sec
                                                                                                              Sequence:
Scoring table:
BLOSUM62
Scoring table:
BLOSUM62
Scoring table:
BLOSUM62
Scoring table:
BLOSUM62
Searched:
Cappe 10.0, Gapext 0.5
Searched:
Adding seqs, 439378781 residues
2443163
Searched:
Adding bloom of hits satisfying chosen parameters:
Minimum DB seq length:
Bost-processing:
Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 100.0%; Score 3135; DB 3; Length 598; Local Similarity 100.0%; Pred. No. 3.8e-190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-DEC-2001.
(GETH ) GENENTECH INC.
(ery Match 100.0%; Score 3135; DB 5; Length 598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 100.0%; Score 3135; DB 3; Length 598; Local Similarity 100.0%; Pred. No. 3.8e-190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUY31844 standard; protein; 598 AA.
Novel human secreted and transmembrane protein PRO357.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 3135; DB 5;
Pred. No. 3.8e-190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Amino acid sequence of novel polypeptide PRO357.
WO200037640-A2.
29-JUN-2000.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY06484 standard; protein; 598 AA.
Human tumour-associated protein PRO357.
WO9935170-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB01322 standard, protein, 598 AA.
Human PR0357 polypeptide.
WQ20032776-A2.
08-JUN-2000
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU81643 standard; protein; 598 AA.
Human PRO protein, Seq ID No 104.
WO200208288-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY93691 standard; protein; 598 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABU55931 standard; protein; 598 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%;
RESULT 5
                                                                                    US-09-943-780-69
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(GETH ) GENENTECH INC.
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                                                                                                       Perfect score:
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                   protein
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RESULT 3
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                                                                                                                                                                                                                                                                          AB033756 standard; protein; 598 AA.
Novel human secreted and transmembrane protein PR0357.
US2003045687-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABUG0352 standard; protein; 598 AA.

Novel human secreted and transmembrane protein PRO357.
US2002168715-A1.
14-NOV-2002.
(GETH ) GENENTECH INC.
ery Match
st Local Similarity 100.0%; Pred. No. 3.8e-190;
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Novel human secreted and transmembrane protein PRO357.
Human secret...
US2002142959-A1.
US2002142959-A1.
03-OCT-2002.
(GETH) GENENTECH INC.
100.0%; Score 3135; DB 6; "Match "lotter" 100.0%; Pred. No. 3.8e-190;
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(GETH ) GENENTECH INC.

100.0%; Score 3135; DB 6;

ATT MATCH 100.0%; Pred. No. 3.8e-190;
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DE Human secreted/transmembrane protein, PRO357.

PN 19-SEP-2002.

PA (GETH ) GENENTECH INC.

Querry Match

Best Local Similarity 100.0%; Pred. No. 3.88-190;
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Pred. No. 3.8e-190;
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Pred. No. 3.8e-190;
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Pred. No. 3.8e-190;
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Pred. No. 3.8e-190;
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Pred. No. 3.8e-190;
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Human secreted/transmembrane protein PRO357.
US2002173463-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABUS8361 standard; protein; 598 AA. Novel human secreted protein PRO357. US2002150976-A1.
                                                                                                                           ABU80790 standard; protein; 598 AA. Human PRO polypeptide #52. US2003036635-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                         ABU60241 standard; protein; 598 AA.
Human PRO polypeptide #12.
US2002132768-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABUS7247 standard; protein; 598 AA.
Human PRO357 protein.
US2002142958-A1.
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21-NOV-2002.
(GETH ) GENENTECH INC.
Warch 100.0%; Sr
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06-MAR-2003.
(GETH ) GENENTECH INC.
Match 'larity 100.0%;
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PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%;
RESULT 12
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03-0CT-2002.
(GETH ) GENENTECH INC.
100.0%;
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Best Local Similarity 100.0%;
RESULT 10
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Query Match

Query Match

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100.0%; Score 3135; DB 7; Length 598; 100.0%; Pred. No. 3.8e-190;
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                                                                                                       ADB78323 standard; protein; 598 AA.
Novel human secreted and transmembrane protein PRO357
US2003092889-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                             ADB78077 standard; protein; 598 AA. Novel human secreted and transmembrane protein PRO357 US2003092886-A1.
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Novel human secreted and transmembrane protein PRO357.
US2003092887-A1.
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Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 32
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Pred. No. 3.8e-190;
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Best Local Similarity 100.0%; Pred. No. 3.8e-190;
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Human secreted/transmembrane PRO polypeptide #12.
US2002142419-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADC25583 standard; protein; 598 AA.
Human secreted/transmembrane PRO polypeptide #12.
US2002156004-A1.
24-OCT-2002.
                                                                                                                                                                                                                                                                  ADB84971 standard; protein; 598 AA.
Human PRO polypeptide #52.
US2003073817-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADB87143 standard; protein; 598 AA. Human PRO polypeptide #52. US2003088067-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADB84725 standard; protein; 598 AA. Human PRO polypeptide #52. US2003092890-A1.
22-MAY-2003.
(GETH ) GENENTECH INC.
100.0%;
                                               Query Match 100.0%;
Best Local Similarity 100.0%;
RESULT 25
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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RESULT 26
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Best Local Similarity
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Human membrane bound receptor/protein PRO357 amino acid sequence
US2003065147-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 598;
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Pred. No. 3.8e-190;
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Novel human secreted and transmembrane protein PRO357.
US2003096968-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADB83594 standard; protein; 598 AA.
Novel human secreted and transmembrane protein PRO357.
US2003073814-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADB80700 standard; protein; 598 AA.
Novel human secreted and transmembrane protein PRO357.
                                                                                                                                                                                                                                                                                                                                                                                                                                           ABJ72279 standard; protein; 598 AA.

Human PRO357 protein.
US2003050448-AL.
U3-MAR-2003.
(GETH) GENENTECH INC.
ery Match
st Local Similarity 100.0%; Pred. No. 3.8e-190;
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US2003088068-A1.
08-MAY-2003.
(GETH ) GENENTECH INC.
100.0%; Score 3135; DB 7;
... Match '1=*ity 100.0%; Pred. No. 3.8e-190;
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(GETH ) GENENTECH INC.
ery Match 100.0%; Score 3135; DB 7;
ery Match 100.0%; Pred. No. 3.8e-190;
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Pred. No. 3.8e-190;
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Pred. No. 3.8e-190;
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Pred. No. 3.8e-190;
                                                                                                                       ABU11313 standard; protein; 598 AA. Human pro357 protein sequence. US2002127643-A1. 12-SEP-2002. (GETH ) GENENTECH INC. 100.0%; Score 3 best Local Similarity 100.0%; Pred. N
                                                                                                                                                                                                                                                                                    ABU67132 standard; protein; 598 AA.
Human PRO polypeptide #12.
US2002165143-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABJ72407 standard; protein; 598 AA Human PR0357 protein. US2003027988-A1. 06-FEB-2003. (GETH ) GENENTECH INC.
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07-NOV-2002.
(GETH ) GENENTECH INC.
werch 100.0%;
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17-APR-2003.
(GETH ) GENENTECH INC.
100.0%;
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                          08-MAY-2003.
(GETH ) GENENTECH INC.
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RESULT 19
ID AB/72407 standard; pr
DE Human PRO357 protein.
PN USZ003027988-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC
                                                                                                                                                                                                                                         Best Local Similarity
RESULT 17
ID ABG7132 standard; pr
DE Human PRO polypeptide
PN US2002165143-A1.
PD 07-NOV-2002.
PA (GETH ) GENENTECH INC
                                                                              Best Local Similarity RESULT 16
                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
RESULT 18
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Best Local Similarity
RESULT 20
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RESULT 24
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Best Local Similarity
RESULT 21
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        US2003088063-A1.
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Query Match

Length 598

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Query Match

Length 598

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RESULT 36

22228

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D AD048807 standard; protein; 598 AA.

Novel human secreted and transmembrane protein PRO357.

W US2003092888-AI.

D 15-MAY-2003.

A (GFTH ) GENENTECH INC.

Query Match

100.0%; Score 3135; DB 8; Length 598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ID ADD51014 standard; protein; 598 AA.

DE Novel human secreted and transmembrane protein PRO357.

PN US2003105290-A1.

PD 05-JUN-2003.

PA (GETH ) GENENTECH INC.

Query Match

Best Local Similarity 100.0%; Pred. No. 3.8e-190;

RESULT 47
                                                          ADD06286 standard; protein; 598 AA.
Novel human secreted and transmembrane protein PRO357.
17-APR-2003.
                                                                                                                                                                                                                     ADC77805 standard; protein; 598 AA.
Novel human secreted and transmembrane protein PRO357.
US2003088066-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AD51260 standard, protein; 598 AA.
Novel human secreted and transmembrane protein PRO357.
US200310289-A1.
05-JUN 2003.
(GFTH ) GENENTECH INC.
(GTT ) ALCh
iery Match
ist Local Similarity 100.0%; Pred. No. 3.8e-190;
                                                                                                                                                                                                                                                                                                                                                                                ADD50768 standard; protein; 598 AA.
Novel human secreted and transmembrane protein PRO357
US2003105291-A1.
    100.0%; Score 3135; DB 7; 100.0%; Pred. No. 3.8e-190;
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Pred. No. 3.8e-190;
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Pred. No. 3.8e-190;
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Pred. No. 3.8e-190;
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Pred. No. 3.8e-190;
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Pred. No. 3.8e-190;
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Pred. No. 3.8e-190;
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RESULT 50

ID ADH27489 standard; protein; 598 AA.

DE Human secreted/transmembrane PRO polypeptide #12.

PN US2003083479-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADD50495 standard; protein; 598 AA. Human PRO polypeptide #52. US2003096971-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein; 598 AA
                                                                                                  PD 08-MAY-2003.

PA (GETH) GENENTECH INC.

Query Match 100.0%;

Best Local Similarity 100.0%;
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01-MAY-2003.
(GETH ) GENENTECH INC.
MATCh ...'1 avity 100.0%;
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d (GETH) GENENTECH INC.
Query Match 100.0%;
Best Local Similarity 100.0%;
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PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%;
RESULT 48
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PA (GETH ) GENENTECH INC.

QUETY MATCh

BBSE Local Similarity 100.0%;

RESULT 49
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US2003096970-Al.
                Best Local Similarity RESULT 43
                                                                                                                                                        Query Match
Best Local Similarity
RESULT 44
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ID ADD51014 Btandard;
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      Query Match
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                    Length 598;
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PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 3135; DB 7; Length 598;

Best Local Similarity 100.0%; Pred. No. 3.88-190;

RESULT 38
                                                                                                                                                                                                                                                                                                                                               Length 598;
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Pred. No. 3.8e-190;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADC49854 standard; protein; 598 AA.
Novel human secreted and transmembrane protein PRO357.
US2003088064-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADC49053 standard; protein; 598 AA.
Novel human secreted and transmembrane protein PRO357.
US2003088070-A1.
(GB-MAY-2003.
(GETH ) GENENTECH INC.
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Novel human secreted and transmembrane protein PRO357.
08-MAY-2003.
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Novel human secreted and transmembrane protein PRO357.
US2003096972-A1.
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Novel human secreted and transmembrane protein PRO357
US2003088072-A1.
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Novel human secreted and transmembrane protein PRO357
US2003105288-A1.
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(GETH ) GENENTECH INC.
(GETH ) GENENTECH INC.
(EFTY Match 100.0%; Score 3135; DB 7;
(ery Match 100.0%; Pred. No. 3.8e-190;
                    Score 3135; DB 7;
Pred. No. 3.8e-190;
                                                            Human secreted/transmembrane PRO polypeptide #12.
US2003077298-Al.
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Human PRO polypeptide #52.
US2003088065-A1.
                100.0%;
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Best Local Similarity 100.0%;
RESULT 37
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(GETH ) GENENTECH INC.
                                                                                                                                   24-APR-2003.
(GETH ) GENENTECH INC.
(GETH ) GENENTECH INC
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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                                                                                                                                                                                          Best Local Similarity RESULT 35
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Best Local Similarity
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                                     Best Local Similarity
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RESULT 41
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Best Local Si
RESULT 42
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                    Query Match
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Best Loc
RESULT 65
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         RESULT 61
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Pred. No. 3.8e-190;
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                                      _ADE20978 standard; protein; 598 AA.
Novel human secreted and transmembrane protein PRO357.
US2003100735-A1.
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Novel human secreted and transmembrane protein PRO357.
US2003100722-A1.
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Novel human secreted and transmembrane protein PRO357.
US2003100738-A1.
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Novel human secreted and transmembrane protein PRO357.
US2003100734-A1.
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Novel human secreted and transmembrane protein PRO357
US2003100717-A1.
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Novel human secreted and transmembrane protein PRO357
US2003096362-A1.
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(Match 100.0%; Score 3135; DB 8;
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(GETH ) GENENTECH INC.
(MATCh 100.0%; Score 3135; DB 8;
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USACCOUNTS.
(GETH ) GENENTECH INC.
(GETH ) GENENTECH INC.
(FINALCH 100.0%; Score 3135; DB 8;
(FINALCH 100.0%; Pred. No. 3.8e-190;
Best Local Similarity 100.0%; Pred. No. 3.8e-190; RESULT 52
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(GETH ) GENENTECH INC.
iry Match 100.0%; Score 3135; DB 8;
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Pred. No. 3.8e-190;
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Pred. No. 3.8e-190;
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US2003100728-A1.
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US2003100727-A1.
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Human PRO polypeptide #52.
US2003100712-A1.
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29-MXY-2003.
(GETH ) GENENTECH INC.
100.0%;
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29-MAY-2003.
(GETH ) GENENTECH INC.
Watch 100.0%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                             Best Local Similarity
RESULT 54
ID ADD75051 standard; p1
DE Human PRO polypeptide
PN US2003100712-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC
                                                                                                                                          Best Local Similarity RESULT 53
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Best Local Similarity
RESULT 55
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RESULT 56
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RESULT 57
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100.0%; Score 3135; DB 8; Length 598; 100.0%; Pred. No. 3.8e-190;
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                                                                                                                                                     ADD78401 standard; protein; 598 AA.
Novel human secreted and transmembrane protein PRO357.
US200310073-A1.
29-MAY-2003.
(GETH ) GENENTECH INC.
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Novel human secreted and transmembrane protein PRO357.
US2003100732-A1.
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Novel human secreted and transmembrane protein PRO357.
US2003100733-A1.
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Novel human secreted and transmembrane protein PRO357
US2003100718-A1.
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Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 64
                                                                                                100.0%; Score 3135; DB 8; 100.0%; Pred. No. 3.8e-190;
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(GETH ) GENENTECH INC.
PRY MATCH 100.0%; Score 3135; DB 8;
st Local Similarity 100.0%; Pred. No. 3.8e-190;
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Human PRO polypeptide #52.
US2003100064-A1.
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ADD73561 standard; protein; 598 AA.
Human PRO polypeptide #52.
US2003100711-A1.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Novel human secreted and transmembrane protein PRO357
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100.0%; Score 3135; DB 8; Length 598;
Beet Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 77
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                                                                         ADD85535 standard; protein; 598 AA.
Novel human secreted and transmembrane protein PRO357.
US2003100721-A1.
PA (GETH) GENERAL BROTELIN; 598 AA.

PD 29-MAY-2003.

PA (GETH) GENENTECH INC.

Query Match

Best Local Similarity 100.0%; Score 3135; DB 8; Len

RESULT 71

ID ADE05084 standard; protein; 598 AA.

PP US2003100726-A1.

PP US2003100726-A1.

PA (FETH) COLUMB BROTELING 
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Novel human secreted and transmembrane protein PRO357.
US2003100715-A1.
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Novel human secreted and transmembrane protein PRO357.
US2003100719-A1.
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Novel human secreted and transmembrane protein PRO357.
US2003100730-A1.
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Novel human secreted and transmembrane protein PRO357
US2003100731-A1.
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Novel human secreted and transmembrane protein PRO357
US2003100729-A1.
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Human secreted/transmembrane PRO polypeptide #12.
US200306742-A1.
22-MAY-2003.
(GETH ) GENENTECH INC.
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Human PRO polypeptide #52.
US2003100714-A1.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
Query Match 1
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 75
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RESULT 78
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Length 598;
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                                                                                                                                                                                                                                                                                                                                                                                                                                ADD77087 standard; protein; 598 AA.
Novel human secreted and transmembrane protein PRO357.
US2003100716-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADD85781 standard; protein; 598 AA.
Novel human secreted and transmembrane protein PRO357.
US2003100720-A1.
29-MAY-2003.
(GETH ) GENENTECH INC.
ery Match
st Local Similarity 100.0%; Pred. No. 3.8e-190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEGOSG17 standard; protein; 598 AA.

BY USCO1309595-A1.

PD 22-MAY-2003.

PA (GETH ) GENENTECH INC.

QUETY MATCh

100.0%; Score 3135; DB 8; Leng

Best Local Similarity 100.0%; Pred. No. 3.8e-190;

RESULT 87

DE HUMAN PRO Polypeptide #52.

PROGOSJ096962-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADG11234 standard; protein; 598 AA. Novel human secreted and transmembrane protein PRO357.
Novel human ...
U3203100725-A1.
29-MAY-2003.
(GETH ) GENENTECH INC.
... Match 100.0%; Score 3135; DB 8; ...
... Match 100.0%; Pred. No. 3.8e-190;
                                                                                                                                                                     PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 81
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(GETH ) GENENTECH INC.
100.0%; Score 3135; DB 8;
lery Match
100.0%; Pred. No. 3.8e-190;
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Pred. No. 3.8e-190;
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Pred. No. 3.8e-190;
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Pred. No. 3.8e-190;
                                                                                                                                                                                                                                                                                    protein; 598 AA.
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Human PRO polypeptide #52.
V US2003100723-A1.
A (GETH ) GENENTECH INC.
OUETY MATCh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADD74805 standard; protein; 598 AA.
Human PRO polypeptide #52.
US2003100724-A1.
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29-MAY-2003.
(GETH ) GENENTECH INC.
100.0%;
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PA (GETH ) GENENTECH INC.
Query Match 100.0%;
Best Local Similarity 100.0%;
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                                                                                                                                                     Human PRO polypeptide #52.
US2003100710-A1.
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US2003100713-A1.
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(GETH ) GENENTECH INC.
                                                                                          Best Local Similarity RESULT 80
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Best Local Similarity
RESULT 86
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                                                                              Query Match
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us-09-943-780-69.ragspdi

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Length 598;
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                                                                                                              ADG12013 standard; protein; 598 AA.
Novel human secreted and transmembrane protein PRO357.
US2003096963-A1.
                                                                                                                                                                                                                                                        ADF94570 standard; protein; 598 AA.
Novel human secreted and transmembrane protein PRO357.
US2003096964-A1.
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US2003096965-A1.
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Novel human secreted and transmembrane protein PRO357
US2004006206-A1.
                                                                                                                                                            C2-MAY-2003.
(GETH ) CENENTECH INC.
(GETH ) CENENTECH INC.
ery Match
100.0%; Score 3135; DB 8;
Admilarity 100.0%; Pred. No. 3.8e-190;
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(GETH ) GENENTECH INC.

(GETH ) GENENTECH INC.

(GETH ) GENENTECH INC.

(GETH ) GENENTECH INC. 3.8e-190;
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(GETH ) GENENTECH INC.
ery Match 100.0%; Score 3135; DB 8;
ery Match 100.0%; Pred. No. 3.8e-190;
                                                          100.0%; Score 3135; DB 8; 100.0%; Pred. No. 3.8e-190;
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(GETH ) GENENTECH INC.
PY MATCH 100.0%; Score 3135; DB 8;
St Local Similarity 100.0%; Pred. No. 3.8e-190;
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Pred. No. 3.8e-190;
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Pred. No. 3.8e-190;
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Human secreted/transmembrane PRO polypeptide #12.
US2003211570-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AD#43210 standard; protein; 598 AA.
Human secreted/transmembrane PRO polypeptide #12.
US2003207401-A1.
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Human PRO polypeptide #52.
US2004019183-A1.
                                                                                                                                                                                                                                                                                                                                                                                               ADG06666 standard; protein; 598 AA.
Human PRO polypeptide #52.
US2003096966-Al.
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Human PRO polypeptide #52.
US2003096960-A1.
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22-MAY-2003.
(GETH ) GENENTECH INC.
100.0%;
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22-MAY-2003.
(GETH ) GENENTECH INC.
""" 100.0%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                         22-MAY-2003, (GETH ) GENENTECH INC.
J-A1.

2003.

.H) GENENTECH.

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Best Local Similarity

RESULT 89

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Best Local Similarity
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Best Le.
RESULT 96
ID ADI3
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PD V
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RESULT 90
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RESULT 94
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AAB07428 standard; protein; 673 AA.
Amino acid sequence of a leucine-rich surface glycoprotein (LRSG).
WO200042170-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADY39535 standard, protein; 598 AA.
Human insulin-like growth factor homolog PRO357 precursor protein
US2005048613-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-MAR-2005.
(GETH ) GENENTECH INC.
(CATH ) GENENTECH INC. 100.0%; Score 3135; DB 9; Length 598;
ery Match 100.0%; Pred. No. 3.8e-190;
                                      Length 598;
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                                                                                                                                                                                                                                                                ADM27222 standard; protein; 598 AA.
Novel human secreted and transmembrane protein PRO357
US2004044179-A1.
(GETH ) GENENTECH INC.
                                                                                                    ADI29825 standard; protein; 598 AA.
Novel human secreted and transmembrane protein PRO357
US2003096961-A1.
PD 29-JAN-2004.

PA (GETH ) GENENTECH INC.

QUENTY MATCh

100.0%; Score 3135; DB 8;

Best Local Similarity 100.0%; Pred. No. 3.8e-190;

RESULT 98
                                                                                                                                                         CGETH ) GENENTECH INC.
(GETH ) GENENTECH INC.

(GETH ) GENENTECH INC.

(GETH ) GENENTECH INC.

(GETH ) GENENTECH INC.
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Pred. No. 3.8e-190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADN00448 standard; protein; 598 AA.
Human secreted/transmembrane PRO polypeptide #12.
US2004091972-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADU25372 standard; protein; 598 AA.
Human secreted/transmembrane PRO polypeptide #12.
US2004220385-A1.
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Pred. No. 1.4e-189;
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Human PRO357 protein, SEQ ID NO: 69
US2005059115-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                      Human PRO polypeptide #52. 08.082004044180-A1.
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Human PRO357 protein sequence.
WO9928462-A2.
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Best Local Similarity 100.0%;
RESULT 105
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GETH ) GENENTECH INC
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                                                                                                                                                                                                                          Best Local Similarity RESULT 99
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20-JUL-2000

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Query Match
(MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
ry Match
98.4%; Score 3083.5; DB 3; Length 673;
t Local Similarity 88.7%; Pred. No. 8.1e-187;
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Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 109
                                                                                                                                                                                                                                                                                                                                                                                        vuery Match
    98.4%; Score 3083.5; DB 5; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 110
                                                                                                                                            Ouery Match 98.4%; Score 3083.5; DB 4; Length 673; Best Local Similarity 88.7%; Pred. No. 8.1e-187;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABU59059 standard; protein; 673 AA.
Novel human secreted or transmembrane protein PRO1282. US2002132252-A1.
                                                                                                                                                                                         AAB65166 standard; protein; 673 AA.
Human PRO1282 (UNQ652) protein sequence SEQ ID NO:52
WO200073454-A1.
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Pred. No. 8.1e-187;
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Pred. No. 8.1e-187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABG78042 standard; protein; 673 AA.
Human leucine-rich surface glycoprotein (LRSG-1).
US2002072089-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 3083.5; DB 5
Pred. No. 8.1e-187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 98.4%; Score 3083.5; DB 5 Local Similarity 88.7%; Pred. No. 8.1e-187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABG95858 standard; protein; 673 AA.
Human secreted/transmembrane protein PRO1282.
US2002119130-A1.
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Human secreted/transmembrane protein PR01282.
US2003012023-A1.
                                                               AAB87533 standard; protein; 673 AA.
Human PR01282.
WO200116318-A2.
                                                                                                                                                                                                                                                                                                                     AAU75266 standard; protein; 673 AA
Human Slit-like protein #1.
WO200212346-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABU57981 standard; protein; 673 AA. Human PRO polypeptide #13. US2003027163-A1. 06-FEB-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HOLT) HOLTZMAN D A. (MCGA/) MCCARTHY S A. (MACB/) MACBETH K J. (BUSF/) BUSFIELD S J. (PANY/) PAN Y. (KHOLY) KHORDOUST M M. (KHON/) KHORDOUST M M.
                                                                                                                                                                                                                                                                                                                                                                     14-FEB-2002.
(PHAA ) PHARMACIA CORP.
                                                                                                                                                                                                                                          07-DEC-2000.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-AUG-2002.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-SEP-2002.
(GETH ) GENENTECH INC.
                                                                                                            08-MAR-2001.
(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 112
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                             Best Local Similarity RESULT 107
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Best Local Similarity
RESULT 113
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Best Local Similarity
RESULT 115
                     Query Match
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ID AA
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RESULT
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ID ABU71313 standard; protein; 673 AA.

DE Human secreted polypeptide PR01282.

PN US2003013855-A1.

PD 16-JAN-2003.

PA (GETH ) GENENTECH INC.

QUETY MATCh

BEST Local Similarity 88.7%; Pred. No. 8.1e-187;

RESULT 122

ID ABU72294 standard; protein; 673 AA.

PN US2002182638-A1.

PN US2002182638-A1.

PN US2002182638-A1.

PA (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                          PD 02-JAN-2003.

PA (GETH ) GENENTECH INC.

Query Match 98.4%; Score 3083.5; DB 6; Length 673;

Best Local Similarity 88.7%; Pred. No. 8.1e-187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 121
                                                                                                                 6; Length 673;
                                                                                                                                                                                                                                                                                                    Score 3083.5; DB 6; Length 673;
Pred. No. 8.1e-187;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98.4%; Score 3083.5; DB 6; Length 673; 88.7%; Pred. No. 8.1e-187;
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                                                                                                                                                                                                                                                                                                                                                     ABU72457 standard; protein; 673 AA.
Novel human secreted and transmembrane protein PRO1282.
US2003003531-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABU71959 standard; protein; 673 AA.
Novel human secreted and transmembrane protein PRO1282
US2003018183-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABU90883 standard; protein; 673 AA.
Novel human secreted and transmembrane protein PRO1282
US2003018173-A1.
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Pred. No. 8.1e-187;
                                                                                                               Score 3083.5; DB 6,
Pred. No. 8.1e-187;
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Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 120
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Human secreted/transmembrane protein PR01282.
US200309013-A1.
(GETH ) GENENTECH INC.
                     Human secreted/transmembrane protein, #19.
ABU60490 standard; protein; 673 AA.
                                                                                                                                                                                ABU13872 standard; protein; 673 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABU59206 standard; protein; 673 AA.
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Best Local Similarity 88.7%; Pi
RESULT 123
ID ABU90967 standard; protein; 673
DE Human PRO polypeptide #8.
PN US2003018168-A1.
PD 23-7AN-2003.
PA (GETH ) GENENTECH INC.
                                                            PD 31-0CT-2002.

PA (GETH ) GENENTECH INC.

QUELY MATCh

Best Local Similarity 88.7%;

RESULT 116
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Best Local Similarity 88.7%;
RESULT 117
                                                                                                                                                                                                        Human PRO1282 polypeptide.
US2002103125-Al.
                                                                                                                                                                                                                                                      01-AUG-2002.
(GETH ) GENENTECH LTD.
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(GETH ) GENENTECH INC.
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                                         US2002160384-A1.
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Score 3083.5; DB 6;
Pred. No. 8.1e-187;
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Human PRO polypeptide #8.
US2003023042-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AB034032 standard, protein, 673 AA.
Human PR01282 polypeptide.
US2003017981-Al.
23-JAN-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                  protein; 673 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABU10827 standard; protein; 673 AA
                                                    protein; 673 AA
                                                                                 US2003v2c.
20-FBB-2003.
(GETH) GENENTECH INC.
98.4%;
     98.4%;
88.7%;
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88.7%;
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US2002123463-A1.
05-SEP-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                             ABU96446 standard; protei
Human PRO polypeptide #8.
US2003027993-A1.
                                                                                                                                                                                                                                   05-DEC-2002.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC
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(GETH ) GENENTECH INC.
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Best Local Similarity
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     Query Match
Best Local Similarity
RESULT 134
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Best Local Similarity
RESULT 143
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Best Local Similarity
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                                                    ABU89275 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JAN-2003
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Pred. No. 8.1e-187;
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                                                                                                                                                                                     6; Length 673;
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                                                    6; Length 673;
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Novel human secreted and transmembrane protein PRO1282.
US2002183493-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABU92290 standard; protein; 673 AA.
Novel human secreted and transmembrane protein PRO1282.
US2003022187-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABO53268 standard; protein; 673 AA.
Novel human secreted and transmembrane protein PRO1282
US2003027986-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABU59355 standard; protein; 673 AA.
Novel human secreted or transmembrane protein PRO1282.
06-FEB-2003.
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Pred. No. 8.1e-187;
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Pred. No. 8.1e-187;
                                                    Score 3083.5; DB 6;
Pred. No. 8.1e-187;
                                                                                                                                                                                                                                  ABO27288 standard; protein; 673 AA.
Human secreted/transmembrane polypeptide PRO1282
US2003009012-A1.
                                                                                                                                                                                    Score 3083.5; DB 6, Pred. No. 8.1e-187;
                                                                                                                                                                                                                                                                                                                                                                 ABU92483 standard; protein; 673 AA.
Human secreted/transmembrane protein PRO1282.
US2003045684-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human sectreted/transmembrane protein, #19 US2002142961-A1.
Human secreted/transmembrane protein, #19
US2003027162-A1.
06-FBB-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABUBI153 standard; protein; 673 AA. Human secreted polypeptide PRO1282. US200302712-A1. GEFB-2003. (GETH.) GENENTECH INC.
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                                                                                                    ABO25903 standard; protein; 673 AA.
                                                                                                                                  US2002...
12-88P-2002.
(GETH ) GENENTECH INC.
98.4%;
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88.7%;
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88.7%;
                                                                                                                 Human PRO1282 polypeptide.
US2002127576-Al.
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(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                 06-MAR-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                     09-JAN-2003.
(GETH ) GENENTECH INC.
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2003.
.H ) GENENTECH 1.
.ty Match
dest Local Similarity PRESULT 128
ID ABU81153 stand>-
DE Human secre'
PN US20030-
PD 06--
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(GETH ) GENENTECH INC.
                                                              Best Local Similarity
RESULT 125
ID AB025903 standard; p
DE Human PR01282 polype;
PN US200212756-A1.
PD 12-SEP-2002.
PA (GETH ) GENENTECH IN
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Best Local Similarity
RESULT 130
ID ABUS8912 standard; p
DE Human sectreted/tran
PN US202142951-A1.
PD 03-GCT-2002.
PA (GETH ) GENENTECH IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
RESULT 131
ID ABU92290 standard; p
DE Novel human secreted
PN US2003022187-A1.
PD 30-UAN-2003.
                                                                                                                                                                                Query Match
Best Local Similarity
RESULT 126
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RESULT 129
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Best Local Similarity
RESULT 133
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Best Local Si
RESULT 127
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Length 673;
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                                                                                                                                                  ABU82482 standard; protein; 673 AA.
Novel human secreted and transmembrane protein PRO1282.
US2002183494-Al.
                                                                                                                                                                                                                                                                                                                             A 28192121 standard; protein; 673 AA.

Novel human secreted and transmembrane protein PRO1282.

US203017476-A1.

22-A701-2003.

98.4%; Score 3083.5; DB 6; Leng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABUSI579 standard; protein; 673 AA.
Novel human secreted and transmembrane protein PRO1282
US2002177164-A1.
Novel human secreted and transmembrane protein PRO1282 US2003036634-A1.
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Human secreted and transmembrane polypeptide PRO1282
US2002197615-A1.
                                                                                                                                                                                                                                                                    98.4%; Score 3083.5; DB 6; 88.7%; Pred. No. 8.1e-187;
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Pred. No. 8.1e-187;
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Pred. No. 8.1e-187;
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Pred. No. 8.1e-187;
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Pred. No. 8.1e-187;
                                                                                      Score 3083.5; DB 6;
Pred. No. 8.1e-187;
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06-FEB-2003.
(GETH ) GENENTECH INC.
(ery Match 98.4%; Score 3083.5; DB 6; Length 673;
      98.4%; Score 3083.5; DB 6; Length 673; 88.7%; Pred. No. 8.1e-187;
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Pred. No. 8.1e-187;
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Pred. No. 8.1e-187;
                                                            ABO34174 standard; protein; 673 AA.
Human secreted/transmembrane polypeptide PRO 1282
US2003060601-A1.
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Human secreted/transmembrane polypeptide PRO 1282
US2003027992-A1.
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Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 159
DD ADA22175 standard; protein; 673 AA.
DE Human secreted/transmembrane polypeptide PRO1282.
PN US2003040473-A1.
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Human secreted/transmembrane PRO polypeptide #13.
US2003049638-A1.
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Human secreted/transmembrane protein PR01282.
USC003044806-A1.
06-MAR-2003.
                                                                                                                                                                                                                    ADA94268 standard; protein; 673 AA.
Human secreted/transmembrane protein PRO1282.
US2003059832-A1.
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Human secreted/transmembrane protein PRO1282.
US2003060407-A1.
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US2003059780-A1.
27-MAR-2003.
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Human secreted/transmembrane protein PRO1282.
US2003017982-A1.
23-JAN-2003.
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Human secreted/transmembrane protein PRO1282.
US2003059782-A1.
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88.7%;
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 158
                      Best Local Similarity RESULT 153
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Best Local Similarity
RESULT 154
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Best Local Similarity
RESULT 161
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Best Local Similarity
RESULT 162
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                                                                                                98.4%; Score 3083.5; DB 6; Length 673; 88.7%; Pred. No. 8.1e-187;
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Pred. No. 8.1e-187;
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Novel human secreted and transmembrane protein PRO1282
US2003069394-A1.
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Novel human secreted and transmembrane protein PRO1282
US2003055222-A1.
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Pred. No. 8.1e-187;
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Human secreted/transmembrane polypeptide PRO 1282.
US2003018172-A1.
23-JAN-2003.
(GETH ) GENENTECH INC.
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Human secreted/transmembrane polypeptide PRO1282
US2003054404-A1.
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Pred. No. 8.1e-187;
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Pred. No. 8.1e-187;
ADB17073 standard; protein; 673 AA.
Human transmembrane PRO polypeptide (SeqID 16).
US2003050462-A1.
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Human transmembrane PRO polypeptide (SeqID 16).
US2003050465-A1.
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Human secreted/transmembrane protein PRO1282.
US2003008297-A1.
09-JAN-2003.
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Human secreted/transmembrane protein PRO1282.
202003054359-A1.
20-MAR-2003.
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Human PRO1282 polypeptide.
US2003054987-A1.
20-MAR-2003.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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RESULT 150
                                                                                                             Best Local Similarity
RESULT 144
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RESULT 146
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RESULT 149
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Novel human secreted and transmembrane protein PRO1282.
US2003073208-A1.
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Novel human secreted and transmembrane protein PRO1282.
US2003138882-A1.
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Novel human secreted and transmembrane protein PRO1282
US2002193299-A1.
                  98.4%; Score 3083.5; DB 7;
88.7%; Pred. No. 8.1e-187;
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Pred, No. 8.1e-187;
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Pred. No. 8.1e-187;
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Pred. No. 8.1e-187;
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88.7%; Pred. No. 8.1e-187;
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                                                                                                                                                                                                                       ADC07240 standard; protein; 673 AA.
Human secreted/transmembrane protein PR01282.
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Human secreted/transmembrane protein PRO1282.
US2003069403-A1.
10-APR-2003.
                                                                       ADC17151 standard; protein; 673 AA. Mammalian PRO polypeptide (SeqID 16) US2003065143-A1. (GETH ) GENENTECH INC.
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Human PRO polypeptide #13.
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(GETH ) GENENTECH INC
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                    Query Match
Best Local Similarity
RESULT 173
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Best Local Similarity
RESULT 175
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RESULT 181
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                                                                                                                              Score 3083.5; DB 7; Length 673; Pred. No. 8.1e-187;
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Pred. No. 8.1e-187;
                                                                                                                                                                                                                                                             7; Length 673;
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                                     ADB85589 standard; protein; 673 AA.
Novel human secreted and transmembrane protein PRO1282.
US2003049735-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADB90892 standard; protein; 673 AA.
Novel human secreted and transmembrane protein PRO1282 US2003083473-A1.
                                                                                                                                                                                                                                                                                                                                                                                                         98.4%; Score 3083.5; DB 7; 88.7%; Pred. No. 8.1e-187;
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Pred. No. 8.1e-187;
     88.7%; Pred. No. 8.1e-187;
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                                                                                                                                                                                                                                                                   Best Local Similarity 88.7%; Score RESULT 165

ID ADB68268 standard; protein; 673 AA. DE Human PRO1282 protein. PU US2003065161-Al. PD 03-APR-2003. PA (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADB68075 standard; protein; 673 AA.
Human PRO1282 protein.
US2003060600-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADC57532 standard; protein; 673 AA.
Human PRO polypeptide #13.
US2003027754-AI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADC54896 standard; protein; 673 AA.
Human PRO polypeptide #13.
US2003045463-A1.
06-MAR-2003.
                                                                                                                                                                                 ADB96060 standard; protein; 673 AA.
Human PRO polypeptide #13.
US2003054403-A1.
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Human PRO polypeptide #13.
US2003064375-Al.
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88.7%;
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88.7%;
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(GETH ) GENENTECH INC.
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US2003060602-A1.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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RESULT 167
ID ADB90892 standard; p1
DE Novel human secreted
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
RESULT 169
ID ADCS4896 standard; pr
DE Human PRO polypeptide
PN US2003045463-A1.
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RESULT 171
ID ADC06972 standard; p1
DE Human PRO1282 protein
PN US200306062-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC
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Best Local Similarity
RESULT 163
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Best Local Similarity
RESULT 164
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Best Local Similarity
RESULT 166
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US2002198148-A1.
                              Length 673;
                                                                                                                      Length 673;
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                                                                                                                                                                                                                                                                                                                       Score 3083.5; DB 7; Length 673; Pred. No. 8.1e-187;
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                                             Novel human secreted and transmembrane protein PRO1282. 17-APR-2003.
                                                                                                                                                Novel human secreted and transmembrane protein PRO1282. US2002193300-A1.
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Novel human secreted and transmembrane protein PRO1282
US2003105298-A1.
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                           98.4%; Score 3083.5; DB 7; 88.7%; Pred. No. 8.1e-187;
                                                                                                                   98.4%; Score 3083.5; DB 7; 88.7%; Pred. No. 8.1e-187;
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Pred. No. 8.1e-187;
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Pred. No. 8.1e-187;
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Pred. No. 8.1e-187;
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Human PR01282 amino acid sequence SEQ ID NO:52.
                                                                                                                                                                                                                                                                ADC82918 standard; protein; 673 AA. Human PRO polypeptide #13. US2003059783-A1. 27-MAR-2003.
                                                                                                                                                                                                                                                                                                                                                            ADD55025 standard; protein; 673 AA. Human PRO polypeptide #13. US2003077593-A1. 24-APR-2003.
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Human PRO polypeptide #13.
US2003077594-Al.
24-APR-2003.
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Human PRO polypeptide #13.
US2002132253-A1.
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88.7%;
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                                                                      (GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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RESULT 188
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Best Local Similarity
RESULT 189
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RESULT 186
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                                   Best Local Similarity RESULT 183
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US2003059833-A1.
27-MAR-2003.
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RESULT 191
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Query Match 98.4%; Score 3083.5; DB 7; Length 673; Best Local Similarity 88.7%; Pred. No. 8.1e-187; RESULT 201
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(GETH) GENENTECH INC.
sry Match 98.4%; Score 3083.5; DB 7; Length 673;
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                                      Score 3083.5; DB 7; Length 673; Pred. No. 8.1e-187;
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                                                                                             ADG01021 standard; protein; 673 AA.
Novel human secreted and transmembrane protein PR01282.
US2003078387-A1.
24-APR-2003.
(GCTH ) GENENTECH INC.
98 44; Score 3083.5; DB 7; Lenget Local Similarity 88.7%; Pred. No. 8.1e-187;
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Novel human secreted and transmembrane protein PRO1282. US2001180795-A1.
                                                                                                                                                                                                                                                  ADG06574 standard; protein; 673 AA.
Novel human secreted and transmembrane protein PRO1282
US2003180793-Al.
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Novel human secreted and transmembrane protein PRO1282
US2003180918-A1.
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Novel human secreted and transmembrane protein PRO1282.
US2003180859-A1.
25-8EP-2003.
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Novel human secreted and transmembrane protein PRO1282.
US2003180904-A1.
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Novel human secreted and transmembrane protein PRO1282
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Novel human secreted and transmembrane protein PRO1282
US2003180919-A1.
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Novel human secreted and transmembrane protein PRO1282
US2003180907-A1.
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Pred. No. 8.1e-187;
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Pred. No. 8.1e-187;
                                    98.4%;
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(GETH) GENENTECH INC.
(GETH) 98.4%;

"Match "lawity 88.7%;
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(GETH ) GENENTECH INC.
26-DEC-2002.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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RESULT 194
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Best Local Similarity
RESULT 195
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RESULT 197
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                                                  Best Local Similarity RESULT 193
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Best Local Similarity
RESULT 196
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(GETH ) GENENTECH INC. 98.4%;
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88.7%;
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88.7%;
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RESULT 216
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Best Local Similarity 88.7%;
RESULT 217
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25-SEP-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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                                           Ouery Match
Best Local Similarity
RESULT 211
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Best Local Similarity
RESULT 214
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                                                                                                                                                                                                                            Human secreted and
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                                                                                                                                                                                                            ADH37931 standard;
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25-SEP-2003.
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                                                          98.4%; Score 3083.5; DB 7; Length 673; 88.7%; Pred. No. 8.1e-187;
                                                                                                                                                                                                                                                                                                  Score 3083.5; DB 7; Length 673; Pred. No. 8.1e-187;
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Novel human secreted and transmembrane protein PRO1282.
US2003180906-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUN14218 standard; protein; 673 AA.

Novel human secreted and transmembrane protein PRO1282.
US2003180914-A1.
25-SEP-2003.
(GETH) GENENTECH INC.
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Novel human secreted and transmembrane protein PRO1282.
US2003180860-A1.
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USA003181643-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADGB5622 standard; protein; 673 AA.
Novel human secreted and transmembrane protein PRO1282 US2003180905-A1.
C5-SEP-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                               Score 3083.5; DB 7;
Pred. No. 8.1e-187;
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Pred. No. 8.1e-187;
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                                                                                                    ADH37414 standard; protein; 673 AA.
Human secreted and transmembrane protein PRO1282.
US2003181646-A1.
25-SEP-2003.
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Human secreted and transmembrane protein PRO1282
US2003181648-A1.
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Human PRO polypeptide #8.
US200180837-A1.
C5-SEP-2003
(GETH ) GENENTECH INC.
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Human PRO polypeptide #8.
US2003180794-A1.
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25-SEP-2003.
(GETH ) GENENTECH INC.
98.4%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                               25-SEP-2003.
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Best Local Similarity
RESULT 209
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Length 673;
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                                                                                                                                                                                                                                                                                                                                                                                                                ADH57351 standard; protein; 673 AA.
Novel human secreted and transmembrane protein PRO1282.
US2003180920-A1.
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Novel human secreted and transmembrane protein PRO1282.
US2003181636-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADH51999 standard; protein; 673 AA. Novel human secreted and transmembrane protein PRO1282
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Novel human secreted and transmembrane protein PRO1282.
US2001181639-A1.
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Novel human secreted and transmembrane protein PRO1282
US2003181696-A1.
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Novel human secreted and transmembrane protein PRO1282
US2003181698-A1.
Score 3083.5; DB 7;
Pred. No. 8.1e-187;
                                                              ADH37754 standard; protein; 673 AA.
Human secreted and transmembrane protein PRO1282.
US2003181647-A1.
25-SEP-2003.
(GETH) GENENTECH INC.
98.4%; Score 3083.5; DB 7;
st Local Similarity 88.7%; Pred. No. 8.1e-187;
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Pred. No. 8.1e-187;
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Pred. No. 8.1e-187;
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Pred. No. 8.1e-187;
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Pred. No. 8.1e-187;
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Pred. No. 8.1e-187;
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98.4%; Score 3083.5; DB 7; Length 673; 88.7%; Pred. No. 8.1e-187;
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                                        ADI25534 standard; protein; 673 AA.
Novel human secreted and transmembrane protein PRO1282
US2003181669-A1.
                                                                                                                                                     ADH97708 standard; protein; 673 AA.
Novel human secreted and transmembrane protein PRO1282 US2003181672-A1.
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Novel human secreted and transmembrane protein PRO1282.
US203181697-A1.
25-SEP-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADH99725 standard; protein; 673 AA.
Novel human secreted and transmembrane protein PRO1282.
US2003049682-A1.
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Novel human secreted and transmembrane protein PRO1282.
US2003181707-A1.
                                                                                                                                                                                                                                                                                                                                                                                    ADI03556 standard; protein; 673 AA.
Novel human secreted and transmembrane protein PRO1282 US2003181656-A1.
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Pred. No. 8.1e-187;
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Pred. No. 8.1e-187;
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Pred. No. 8.1e-187;
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Pred. No. 8.1e-187;
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Pred. No. 8.1e-187;
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Pred. No. 8.1e-187;
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Pred. No. 8.1e-187;
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US2003181686-A1.
25-SEP-2003.
iry Match
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Human PRO polypeptide #13.
US22003050457-A1.
13-MAR-2003.
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Human PRO polypeptide #8.
US2003181682-A1.
                                                                                                                  98.4%;
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RESULT 229
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88.7%;
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Local Similarity 88.7%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 222
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Best Local Similarity
RESULT 223
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Best Local Similarity
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RESULT 220
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Best Local Similarity
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Query Match
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RESULT 224
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Query Match 98.4%; Score 3083.5; DB 7; Length 673; Best Local Similarity 88.7%; Pred. No. 8.1e-187; RESULT 232
                                                                                             Score 3083.5; DB 7; Length 673; Pred. No. 8.1e-187;
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Novel human secreted and transmembrane protein PRO1282.
US2003181673-A1.
25-S203.
(GETH) GENENTECH INC.
98.4%; Score 3083.5; DB 7; Lengery Match
st Local Similarity 88.7%; Pred. No. 8.1e-187;
                                                                                                                                                                                                                                                                                                     ADH98558 standard; protein; 673 AA.
Novel human secreted and transmembrane protein PRO1282
US2003181708-A1.
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Novel human secreted and transmembrane protein PRO1282.
US2003180848-A1.
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Novel human secreted and transmembrane protein PRO1282.
US203181657-A1.
25-SE2-2003. (GETH ) GENENTECH INC.
                                                                                                                                                 ADH98218 standard; protein; 673 AA.
Novel human secreted and transmembrane protein PRO1282
US2003181709-A1.
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Novel human secreted and transmembrane protein PRO1282
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Novel human secreted and transmembrane protein PRO1282
US2003181676-A1.
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GENENTECH INC.
h
Similarity 88.7%; Pred. No. 8.1e-187;
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Pred. No. 8.1e-187;
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Pred. No. 8.1e-187;
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Pred. No. 8.1e-187;
ADI11573 standard; protein; 673 AA.
Human PRO polypeptide #8.
US2003181684-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADH78235 standard; protein; 673 AA-Human PRO polypeptide #8.
US2003181668-AA.
C5-SEP-2003.
(GETH ) GENENTECH INC.
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25-SEP-2003.
(GETH ) GENENTECH INC.
98.4%;
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PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 88.7%;
                                             PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%;
Best Local Similarity 98.7%;
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 234
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Best Local Similarity
RESULT 235
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(GETH ) GEN
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Length 673;

Length 673;

Length 673;

DB 7;

Length 673;

Length 673;

Length 673;

Length 673;

Length 673;

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Novel human secreted and transmembrane protein PR01282. US2003181677-A1. 25-SEP-2003. (GETH ) GENENTECH INC.
                                                                                       Novel human secreted and transmembrane protein PRO1282. US200316741.
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Novel human secreted and transmembrane protein PRO1282
US2003191290-A1.
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Novel human secreted and transmembrane protein PRO1282
US2003181678-A1.
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Novel human secreted and transmembrane protein PRO1282
US2003181679-Al.
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Novel human secreted and transmembrane protein PRO1282.
US2003181680-A1.
25-SEP-2003.
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Novel human secreted and transmembrane protein PRO1282.
US2003191289-A1.
                                                                                                                                                                                                                                                                                                                                                                             ADI19409 standard; protein; 673 AA.
Novel human secreted and transmembrane protein PRO1282
US2003181675-A1.
                                                   Score 3083.5; DB 7;
Pred. No. 8.1e-187;
                                                                                                                                                                                         98.4%; Score 3083.5; DB 7; 88.7%; Pred. No. 8.1e-187;
                                                                                                                                                                                                                                                                                                                               Score 3083.5; DB 7;
Pred. No. 8.1e-187;
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Pred. No. 8.1e-187;
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Pred. No. 8.1e-187;
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Pred. No. 8.1e-187;
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Pred. No. 8.1e-187;
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25-SEP-2003.
(GETH) GENENTECH INC.
98.4%; S
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                 25-SEP-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Query Match
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Best Local Similarity
RESULT 253
                                                                Best Local Similarity RESULT 248
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                                                                                                                                                                                                         Best Local Similarity
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ID ADI05210 standard;
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   US2003181685-A1.
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(GETH ) GEN
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(GETH) GENENTECH INC.
ery Match
ery Match
-- ronal Similarity 88.7%; Pred. No. 8.1e-187;
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Novel human secreted and transmembrane protein PRO1282. US2003181699-A1.
                                                                                                                   ADI03046 standard; protein; 673 AA.
Novel human secreted and transmembrane protein PRO1282
US2003181653-A1.
                                                                                                                                                                                                                                                                                                                                                                                         ADH97878 standard; protein; 673 AA.
Novel human secreted and transmembrane protein PRO1282.
US2003181674-A1.
25-SEP-2003.
(GETH ) GENENTECH INC.
98.4%; Score 3083.5; DB 7; Lence tocal Similarity 88.7%; Pred. No. 8.1e-187;
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Novel human secreted and transmembrane protein PRO1282.
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Novel human secreted and transmembrane protein PRO1282.
US2003181650-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADI01958 standard; protein; 673 AA.
Novel human secreted and transmembrane protein PRO1282
US2003181652-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADI03216 standard; protein; 673 AA.
Novel human secreted and transmembrane protein PRO1282
US2003181655-A1.
                                                                                                                                                                                                         Score 3083.5; DB 7;
Pred. No. 8.1e-187;
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Pred. No. 8.1e-187;
                                                                   Score 3083.5; DB 7
Pred. No. 8.1e-187;
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Pred. No. 8.1e-187;
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US2003181666-A1.
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Human PRO polypeptide #8.
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25-SEP-2003.
(GETH ) GENENTECH INC.
98.4%; SC
                81695...
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) GENENTECH INC.
98.4%; S
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25-SEP-2003.
(GETH ) GENENTECH INC.
Match '72-ity 88.7%;
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09-007-2003.
(GETH ) GENENTECH INC.
MALCh '12-tity 88.7%;
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88.7%;
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Best Local Similarity
RESULT 241
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Best Local Similarity
RESULT 246
                                                                                Local Similarity
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RESULT 244
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Best Local Similarity
RESULT 247
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Best Local Similarity
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                                 25-SEP-2003
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Best Local Si
RESULT 239
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Length 673;

Length 673;

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RESULT 264

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Score 3083:5; DB 8; Length 673; Pred. No. 8.1e-187;
(GETH ) GENENTECH INC.

17 Match 98.4%; Score 3083.5; DB 7; Length 673; 18 Accal Similarity 88.7%; Pred. No. 8.1e-187;
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3 Human PRO polypeptide #8.

4 US2003181645-A1.

5 25-SEP-2003.

4 (GETH ) GENENTECH INC.

98.4%; Score 3083.5; DB 8; Length 673;
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                                                                                 ADC52154 standard; protein; 673 AA.
Novel human secreted and transmembrane protein PRO1282.
US2003130483-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADH06586 standard; protein; 673 AA.
Novel human secreted and transmembrane protein PRO1282.
US2003180852-A1.
25-SEP-2003.
(GETH) GENENTECH INC.
98.4%; Score 3083.5; DB 8; Lenget Local Similarity 88.7%; Pred. No. 8.1e-187;
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Novel human secreted and transmembrane protein PRO1282
US2003180853-A1.
25-SEP-2003.
(GETH ) GENENTECH INC.
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Novel human secreted and transmembrane protein PRO1282
US2003180855-A1.
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Novel human secreted and transmembrane protein PRO1282
US2003180912-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADH25068 standard; protein; 673 AA.
Novel human secreted and transmembrane protein PRO1282.05203180913-A1.
25-SEP-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                            Score 3083.5; DB 8;
Pred. No. 8.1e-187;
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Pred. No. 8.1e-187;
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Pred. No. 8.1e-187;
                                                                                                                                                                                                                                                                                                                                                              ADG11428 standard; protein; 673 AA.
Human PRO1282 polypeptide.
US2003228655-A1.
11-DEC-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                ADF35178 standard; protein; 673 AA.
Human PRO1282 polypeptide.
US2003194760-A1.
16-OCT-2003.
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(GETH ) GENENTECH INC.
                                          Best Local Similarity
RESULT 266
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RESULT 267
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RESULT 270
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Best Local Similarity
RESULT 271
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                                          98.4%; Score 3083.5; DB 7; Length 673; 88.7%; Pred. No. 8.1e-187;
                                                                                                                                                                                            Score 3083.5; DB 7; Length 673; Pred. No. 8.1e-187;
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                                                                                           ADI04610 standard; protein; 673 AA.
Novel human secreted and transmembrane protein PRO1282.
US2003171550-A1.
11-SEP-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                   ADJUZ746 standard; protein; 673 AA.
Novel human secreted and transmembrane protein PRO1282. US2002181651-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADI25704 standard; protein; 673 AA.
Novel human secreted and transmembrane protein PRO1282
US2003181670-A1.
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Novel human secreted and transmembrane protein PRO1282.
US2003181671-A1.
25-SEP-2003.
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Novel human secreted and transmembrane protein PRO1282
US2003073821-Al.
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Novel human secreted and transmembrane protein PRO1282
US2003191284-A1.
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Novel human secreted and transmembrane protein PRO1282.
US2003040013-A1.
27-PEB-2003.
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Novel human secreted and transmembrane protein PR01282
US2003191287-A1.
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Pred. No. 8.1e-187;
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Pred. No. 8.1e-187;
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Pred. No. 8.1e-187;
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                                                                                                                                                                                                                                                                                                                                                                                                 ADH78065 standard; protein; 673 AA.
Human PRO polypeptide #8.
US2003181667-A1.
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25-SEP-2003.
(GETH ) GENENTECH INC.
98.4%; SC
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25-SEP-2003.
(GETH ) GENENTECH INC.
98.4%; Sr
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88.7%;
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88.7%;
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 09-OCT-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 260
ID AD125704 standard; pro
DE Novel human secreted a
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC
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(GETH ) GENENTECH INC
                                                        Best Local Similarity RESULT 257
                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity RESULT 259
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Best Local Similarity
RESULT 258
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RESULT 263
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Best Local S:
RESULT 265
                                            Query Match
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Human PRO polypeptide #8.
US2003181644-A1.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC
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RESULT 288
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Best Local Similarity
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Best Local Similarity
RESULT 293
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                                                                                                                   Score 3083.5; DB 8; Length 673; Pred. No. 8.1e-187;
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Novel human secreted and transmembrane protein PRO1282.
US2003180846-A1.
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                                                                                                                                                                  ADH07950 standard; protein; 673 AA.
Novel human secreted and transmembrane protein PRO1282
US2003180845-A1.
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Novel human secreted and transmembrane protein PRO1282
US2003180917-A1.
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Novel human secreted and transmembrane protein PRO1282
US2003166848-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADH06246 standard, protein, 673 AA.
Novel human secreted and transmembrane protein PR01282 US2003180854-A1.
C5-SEP-2003 (GETH ) GENENTECH INC.
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Pred. No. 8.1e-187;
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Pred. No. 8.1e-187;
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Pred. No. 8.1e-187;
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Pred. No. 8.1e-187;
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 88.7%; Pred. No. 8.1e-187;
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Human secreted/transmembrane protein PRO1282.
US2003228656-A1.
                                 ADH02343 standard; protein; 673 AA.
Human PRO polypeptide #8.
US2003180839-A1.
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25-SEP-2003.
(GETH ) GENENTECH INC.
98.4%;
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25-SEP-2003.
(GETH ) GENENTECH INC.
98.4%;
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11-DEC-2003.
(GETH ) GENENTECH INC.
98.4%;
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88.7%;
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88.7%;
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88.7%;
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US2003180842-A1.
25-SEP-2003.
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(GETH ) GENENTECH INC.
                                                                                25-SEP-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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RESULT 278
ID ADH39168 standard, p.
DE Novel human secreted
PN US200180917-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH IN
Best Local Similarity RESULT 275
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Best Local Similarity
RESULT 282
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Best Local Similarity
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Best Local Similarity
RESULT 277
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RESULT 279
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Length 673;
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RESULT 284

ID ADH24388 standard; protein; 673 AA.

DE Novel human secreted and transmembrane protein PRO1282.

PN US2003180910-A1.

PD 25-SEP-2003.

PA (GETH ) GENENTECH INC.
                                                                                                                                           ADG69517 standard; protein; 673 AA.
Novel human secreted and transmembrane protein PRO1282.US203180844-A1.
25-SEP-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                            ALHO7780 standard; protein; 673 AA.
Novel human secreted and transmembrane protein PRO1282.
US2001180851-A1.
                                                                                                                                                                                                                                                                                                                                                                                                      ADG85792 standard; protein; 673 AA.
Novel human secreted and transmembrane protein PRO1282.
US2003180861-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADH39338 standard; protein; 673 AA.
Novel human secreted and transmembrane protein PRO1282 US2003180916-A1.
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Novel human secreted and transmembrane protein PRO1282
US2003180843-A1.
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Pred. No. 8.1e-187;
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Pred. No. 8.1e-187;
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Pred. No. 8.1e-187;
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Pred. No. 8.1e-187;
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Pred. No. 8.1e-187;
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US2003180838-A1.
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25-SEP-2003.
(GETH ) GENENTECH INC.
98.4%; St
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88.7%;
                                                                                           Best Local Similarity 88.7%;
RESULT 285
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Best Local Similarity 88.7%;
RESULT 287
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25-SEP-2003.
(GETH ) GENENTECH INC.
    US2003180850-A1.
                                                Query Match
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Novel human secreted and transmembrane protein PRO1282.
US2003180847-A1.
25-SEP-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                ADG85962 standard; protein; 673 AA.
Novel human secreted and transmembrane protein PRO1282.
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Novel human secreted and transmembrane protein PRO1282.
US203180849-A1.
25-SEP-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADH24898 standard; protein; 673 AA,
Novel human secreted and transmembrane protein PRO1282
US2003180909-A1.
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Novel human secreted and transmembrane protein PRO1282
US2003180915-A1.
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Novel human secreted and transmembrane protein PRO1282.
                                                          Score 3083.5; DB 8;
Pred. No. 8.1e-187;
                                                                                                                                                                                Score 3083.5; DB 8;
Pred. No. 8.1e-187;
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Pred. No. 8.1e-187;
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Pred. No. 8.1e-187;
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ADH20791 standard; protein; 673 AA.
Human secreted/transmembrane protein PRO1282.
US2003224358-A1.
04-DEC-2003.
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Human secreted/transmembrane protein PRO1282.
US2003219856-A1.
                                                                                                 ADM02173 standard; protein; 673 AA.
Human PRO polypeptide #8.
US2001180841-A1.
25-SED-2003.
(GETH ) GENENTECH INC.
Query Match
Best Local Similarity 88.7%; Pred. No
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Human PRO polypeptide #8.
US2003180840-A1.
                                                             98.4%;
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88.7%;
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RESULT 301
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88.7%;
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JEP-2003.
(GETH) (GENENTECH IN Query Match BENEL Local Similarity 8. RESULT 295
ID ADG69177 standar PN USCO31" PN LSCO31" PN PD 25-"
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(GETH ) GENENTECH INC.
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25-SEP-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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                                                                        Best Local Similarity
RESULT 294
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RESULT 297
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ID ADH38342 standard; protein; 673 AA.

DE Novel human secreted and transmembrane protein PRO1282.

PN US2003180922-A1.

PD 25-SEP-2003.

PA (GETH) GENENTECH INC.

Query Match

Best Local Similarity 88.7%; Pred. No. 8.1e-187;

RESULT 307
                                                                                                                                                                                                                           ID ADH24728 standard; protein; 673 AA.

DE Novel human secreted and transmembrane protein PRO1282.

PN US2003180908-A1.

PD 25-SEP-2003.

PA (GETH ) GENENTECH INC.

Query March

Best Local Similarity 88.7%; Pred. No. 8.1e-187;

RESULT 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACH52169 standard; protein; 673 AA.

Novel human secreted and transmembrane protein PRO1282.
US2003180921-A1.
25-E2003.
(GETH ) GENENTECH INC.
98.4%; Score 3083.5; DB 8; Length 673; Bt Local Similarity 88.7%; Pred. No. 8.1e-187;
98.4%; Score 3083.5; DB 8; Length 673; 88.7%; Pred. No. 8.1e-187;
                                                                                                                                                                      Length 673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 3083.5; DB 8; Length 673; Pred. No. 8.1e-187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 673;
                                                                                                                                                                                                                                                                                                                                                                                  Novel human secreted and transmembrane protein PRO1282.
US2002180911-A1.
                                                                              Novel human secreted and transmembrane protein PRO1282 US203180863-A1. 25-SEP-2003. (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADH57181 standard; protein; 673 AA.
Novel human secreted and transmembrane protein PRO1282.
US2003181642-A1.
25-SEP-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADH49535 standard; protein; 673 AA.
Novel human secreted and transmembrane protein PRO1282
US2003180857-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADH90497 standard; protein; 673 AA.
Novel human secreted and transmembrane protein PRO1282.
US2003181700-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-SEP-2005.
(GETH ) GENENTECH INC.
2ry Match 98.4%; Score 3083.5; DB 8;
2ry Match 98.7%; Pred. No. 8.1e-187;
                                                                                                                                                                    Score 3083.5; DB 8;
Pred. No. 8.1e-187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 3083.5; DB 8;
Pred. No. 8.1e-187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 3083.5; DB 8 Pred. No. 8.1e-187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human PRO polypeptide #8.
US2003181683-A1.
                                                              protein; 673 AA
                                                                                                                                                            Best Local Similarity 88.7%;
RESULT 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PD 25-SEP-2003.

PA (GETH ) GENENTECH INC.

QUERY MARCH

Best Local Similarity 88.7%;

RESULT 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 98.4%;
Best Local Similarity 88.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-SEP-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-SEP-2003.
(GETH ) GENENTECH INC.
               Best Local Similarity RESULT 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity RESULT 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity RESULT 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity RESULT 310
                                                          ADG86132 standard;
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Length 673;

Length 673;

Length 673;

Length 673;

Length 673;

Length 673;

Query Mat Best Loca RESULT 313

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Score 3083.5; DB 9; Length 673; Pred. No. 8.1e-187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADR45587 standard; protein; 673 AA.
Human leucine-rich surface glycoprotein, LRSG-1, protein #1.
US2004176296-A1.
09-SEP-2004.
(MILL-) MILLENNIUM PHARM INC.
                                                                                 ADH79041 standard; protein; 673 AA.
Novel human secreted and transmembrane protein PRO1282.
US2003181702-A1.
25-SEP-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                               ADKI4422 standard; protein; 673 AA.
Novel human secreted and transmembrane protein PRO1282
US2003187229-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB84689 standard; protein; 673 AA.
Amino acid sequence of human slit polypeptide zslit3.
WO200146418-A1.
28-UUN-2011.
(ZYMO ) ZYMOGENETICS INC.
   (GETH ) GENENTECH INC.
2ry Match 98.4%; Score 3083.5; DB 8;
2. 7.2.7 Similarity 88.7%; Pred. No. 8.1e-187;
                                                                                                                                                                                98.4%; Score 3083.5; DB 8; 88.7%; Pred. No. 8.1e-187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 3083.5; DB 8;
Pred. No. 8.1e-187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98.4%; Score 3083.5; DB 8; 88.7%; Pred. No. 8.1e-187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 3083.5; DB 9;
Pred. No. 8.1e-187;
                                                                                                                                                                                                                                                                                                                              98.4%; Score 3083.5; DB 8; 88.7%; Pred. No. 8.1e-187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 3083.5; DB 8;
Pred. No. 8.1e-187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neoplastic disease detection protein PR01282. WS2005059102-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human secreted/transmembrane protein, #81
US2005112725-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein; 673 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AEA38367 standard; protein; 673 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98.4%;
                                                                                                                                                                                                                                                        Human PRO polypeptide #8.
US2003186407-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (EATO/) EATON D L.
(FILV/) FILWAROFF E.
(GERV) GERRITSEN M E.
(GODD/) GODDARD A.
(GODO/) GODOWSKI P J.
(GRIM/) GRIMALDI J C.
(GRIM/) GRIMALDI J C.
(GRIM/) GRIMEY A L.
(WATA/) WATAANABE C K.
(WOOD/) WOOD W I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-MAR-2004.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-MAY-2005.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                             (GETH ) GENENTECH INC
                                Query Match
Best Local Similarity
RESULT 321
                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                         Best Local Similarity RESULT 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity RESULT 327
                                                                                                                                                                                                                                   ADK00901 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                            02-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                        02-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query
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PA (GETH) GENENTECH INC.

Query Match 98.4*; Score 3083.5; DB 8; Length 673;

Best Local Similarity 88.7*; Pred. No. 8.1e-187;

RESULT 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 673;
                                                                                                                                                                                                                                                                                                                                                 Length 673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98.4%; Score 3083.5; DB 8; Length 673; 88.7%; Pred. No. 8.1e-187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98.4%; Score 3083.5; DB 8; Length 673; 88.7%; Pred. No. 8.1e-187;
                                                                                                                                                                                                   Length 673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 3083.5; DB 8; Length 673; Pred. No. 8.1e-187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADJ98893 standard; protein; 673 AA.
Novel human secreted and transmembrane protein PRO1282.
US2003187242-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUNICEVI Standard; protein; 673 AA.
Novel human secreted and transmembrane protein PRO1282.
052003181703-A1.
                                                                                                                                                                                                                                                    ADI02128 standard; protein; 673 AA.
Novel human secreted and transmembrane protein PRO1282
US2003190699-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADJ99105 standard; protein; 673 AA.
Novel human secreted and transmembrane protein PRO1282.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADJ99275 standard; protein; 673 AA.
Novel human secreted and transmembrane protein PRO1282
US2003187196-A1.
                                                                                                                                                                                                                                                                                                                                                                                                ADH90667 standard; protein; 673 AA.
Novel human secreted and transmembrane protein PRO1282
US2003181701-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADJ89712 standard; protein; 673 AA.
Novel human secreted and transmembrane protein PRO1282
US2003187228-A1.
                                                                                                      ADH98898 standard; protein; 673 AA.
Novel human secreted and transmembrane protein PRO1282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADJ98542 standard; protein; 673 AA.
Novel human secreted and transmembrane protein PRO1282
US2003187197-A1.
                                                                                                                                                                                                 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 3083.5; DB 8;
Pred. No. 8.1e-187;
                                                                                                                                                                                                                                                                                                                                                 .,
8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 3083.5; DB 8;
Pred. No. 8.1e-187;
                                                                                                                                                                09-CCT-zuus.
(GETH ) GENENTECH INC.
:ry Match 98.4%; Score 3083.5; DB 8;
rry Match 98.7%; Pred. No. 8.1e-187;
                                                                                                                                                                                                                                                                                                                                               Score 3083.5; DB 8,
Pred. No. 8.1e-187;
                                                                                                                                                                                                                                                                                                                                                                                                                                      S2003101.
25-SEP-2003.
(GETH) GENENTECH INC.
98.4%;
                                                                                                                                                                                                                                                                                                         09-OCT-2003.
(GETH ) GENENTECH INC.
FRY MATCh 98.4%;
St Local Similarity 88.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98.4%;
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25-SEP-2003.
(GETH ) GENENTECH INC.
Match '12-rity 88.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-OCT-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-OCT-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-OCT-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-OCT-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
RESULT 316
ID ADJ98712 standard; pr
DE Novel human secreted
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
RESULT 317
ID ADH78871 standard; pr
DE Novel human secreted
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
RESULT 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
RESULT 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity RESULT 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                            US2003190698-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US2003186408-A1.
                                                                                                                                                             09-OCT-200
                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Si
RESULT 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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Query

RESULT 330

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W02003029437-A2.
10-APR-2003.
(INCY-) INCYTE GENOMICS INC.
Query Match 31.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-JUN-2003.
(INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAN Y.
WHITE D.
KHODADOUST M M.
                                                                                                                                                                                                                                                                                                                                            HOLTZMAN D A. MCCARTHY S A. MACBETH K J. BUSFIELD S J.
                                                                                                     (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
RESULT 342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match
Local Similarity
                                                                                                                                       Query Match
Best Local Similarity
RESULT 338
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RESULT 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                        (MCCA/)
(MACB/)
(BUSF/)
(PANY/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (WHIT/)
(KHOD/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB38400 standard; peptide; 723 AA.
Fragment of human secreted protein encoded by gene 3 clone HSYAVSO.
WO200061623-A1.
                                                                                                     98.2%; Score 3078.5; DB 4; Length 673; 88.6%; Pred. No. 1.7e-186;
                                                                                                                                                                                                                                                                                                                                   Score 3078.5; DB 7; Length 673; Pred. No. 1.7e-186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98.2%; Score 3078.5; DB 8; Length 676; 88.6%; Pred. No. 1.7e-186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 630;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 672;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93.6%; Score 2935; DB 6; Length 672; 85.2%; Pred. No. 2.1e-177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 672;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93.6%; Score 2935; DB 3; Length 723; B5.2%; Pred. No. 2.2e-177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93.6%; Score 2935; DB 3; Length 673, 85.2%; Pred. No. 2.1e-177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB38323 standard; protein; 673 AA.
Human secreted protein encoded by gene 3 clone H8YAV50
WO200061623-A1.
19-OCT-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93.6%; Score 2935; DB 6;
85.2%; Pred. No. 2.1e-177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 2845.5; DB 5
Pred. No. 8.9e-172;
                                                                                                                                                                                                                                                                                                                                                                                                                            ABO59449 standard; protein; 676 AA.
Human genome derived single exon protein #5683.
US2003194704-A1.
                                                                                                                                                                                     ADF69108 standard; protein; 673 AA. Human MP33 protein sequence SEQ ID NO:78. 09-0cT-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADA57213 standard; protein; 672 AA.
Human secreted protein #496.
WO2002102994-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU75267 standard; protein; 630 AA.
Human Slit-like protein #2.
WO200212346-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADA11092 standard; protein; 672 AA. Human secreted protein. WO2002102993-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABR47923 standard; protein; 672 AA.
Human secreted protein, SEQ ID 814
WO200295010-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY66643 standard; protein; 611 AA Membrane-bound protein PR01282.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PD 19-0CT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 93.6%; &
Best Local Similarity 85.2%; F
RESULT 336
                                                                                                                                                                                                                                                                                                                                         98.2%;
88.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-DEC-2002.
(HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-NOV-2002.
(HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90.8%;
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Lry Match
Beet Local Similarity
RESULT 329
ID ADF69108 stand*
DB Human MP53
PN W020030*
PD 09-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                (EXEL-) EXELIXIS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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Best Local S
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2226

PPRE

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ADA00753 standard; protein; 673 AA.
Murine stromal cell derived haematopoietin factor-5 SEQ ID NO:10.
Wor2003018805-A1.
66-MAR-2003.
(NISC-) JAPAN SCI & TECHNOLOGY CORP.
(NINA-) JAPAN NAT CANCER CENT.
ery Match
ety Match

Et Local Similarity 73.4%; Pred. No. 7.7e-149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA030821 standard; protein; 117 AA.
Human cell adhesion and extracellular matrix protein (CADECM)-11.
WO2003047526-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 37.6%; Score 1178.5; DB 5; Length 281; Best Local Similarity 80.7%; Pred. No. 1.4e-66; RESULT 343
86.5%; Score 2712.5; DB 3; Length 611; 79.5%; Pred. No. 2.3e-163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABRS8506 standard; protein; 307 AA.
Human secreted protein Incyte ID No: 7500228CD1 SEQ ID NO: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADR45596 standard; protein; 673 AA.
Human leucine-rich surface glycoprotein, LRSG-1, protein #2.
US2004176296-A1.
09-SEP-2004.
(MILL-) MILLENNIUM PHARM INC.
19.4#; Score 2490; DB 8; Length 673; st Local Similarity 73.5#; Pred. No. 3.2e-149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 493;
                                                                                                                                                                                                                                                                                                                                                                                         Length 673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB72324 standard; protein; 281 AA.
Rat protein isolated from skin cells SEQ ID NO: 648.
WQ200190357-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08 7;
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                                                                             ABG78046 standard; protein; 673 AA.
Mouse leucine-rich surface glycoprotein (LRSG-1).
US2002072089-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-JUL-2000.
(MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
ery Match 53.3%; Score 1672; DB 3;
                                                                                                                                                                                                                                                                                                                                                                                         79.4%; Score 2490; DB 5; 73.5%; Pred. No. 3.2e-149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31.8%; Score 997.5; DB 768.7%; Pred. No. 4.6e-55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A leucine-rich surface glycoprotein (LRSG) A2. A 200042170-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA030403 standard; protein; 311 AA. Human secreted protein (SECP)-6. WO2003046196-A1. CS-JUN-2003. (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-NOV-2001.
(GENE-) GENESIS RES & DEV CORP LTD.
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Query Match
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Lugth 117;

Lu 04-APR-2002.

PA (ELIL ) LILLY & CO ELI.

Query Match

RESUL ) Lilly & CO ELI.

Query Match

RESUL ) Lilly & CO ELI.

RESULT 347

ID ABP70142 standard; protein; 647 AA.

PN WO200272771-A2.

PD 19-SEP-200?

PA (FILL ) LILLY & CO ELI.

Best Local Similarity 27.1%; Pred. No. 2.4e-14;

RESULT 347

ID ABP70142 standard; protein; 647 AA.

PN WO200272771-A2.

PD 19-SEP-200?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OS-DEC-2002.

(INCY-) INCYTE GENOMICS INC.

ery Match 11.5%; Score 359.5; DB 6; Length 635; and the continuity 27.6%; Pred. No. 2.8e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.5%; Score 360.5; DB 5; Length 647; 27.1%; Pred. No. 2.5e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 778;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 350.5; DB 8; Length 545;
Pred. No. 8.7e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 9; Length 635;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.4%; Score 357.5; DB 5; 26.7%; Pred. No. 4.8e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 27.6%; Pred. No. 2.8e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADM90979 standard; protein; 545 AA.
Human pharmaceutically useful protein SeqID 372
WO2004020595-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 339; DB 5;
Pred. No. 4.9e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE17484 standard; protein; 551 AA.
Human leucine-rich repeat-8 (ZLRR8) protein #2.
WO2002604-A2.
(ZNW ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADZ09859 standard; protein; 635 AA.
Human breast cancer marker MGC3103 protein.
EB1522594-22.
13-APR-2005.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAO26256 standard; protein; 635 AA.
MDDT related human protein SEQ ID No 34.
WO200296951-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-MAR-2004.
(FIVE.) FIVE PRIME THERAPEUTICS INC.
(RIKE.) RIKEN INST PHYSICAL & CHEM RES.
(DNAF.) DNAFORM KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABP70144 standard; protein; 778 AA. Human NOV44c. WO20072771-A2. (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABP70143 standard; protein; 566 AA.
Human NOV44b.
WO200272771-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADI21104 standard; protein; 618 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.8%;
26.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 11.2%;
Local Similarity 27.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel human protein #79.
WO2003025148-A2.
27-MAR-2003.
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(CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
RESULT 348
ID AAO26256 standard; pi
DE MDDT related human pi
Pi WO200296951-A1.
PD 05-DEC-2002.
PA (INCY-) INCYTE GENOMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity RESULT 350
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Best Local Similarity
RESULT 353
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(CURA-)
QUETY MATCH
BEST LOCAL S:
RESULT 351
ID ADM9097
DE HUMAN
PN WO20
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Best Local Si
RESULT 354
ID AD121104 8
DE Novel huma
PN WO20030251
PD 27-MAR-200
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Best Loca
RESULT 352
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CO-MAR-2003.

(SHIM/) SHIMKETS R A.

(SHIM/) SHIMKETS R A.

(IMACO) LAROCHELLE W J.

Query Match

Best Local Similarity 25.8%; Pred. No. 1.2e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-DEC-1999.
(GETH ) GENENTECH INC.
lery Match 10.5%; Score 330; DB 3; Length 653;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-071-1999.
(GEMY ) GENETICS INST INC.
(GEMY ) MAtch 10.5%; Score 330; DB 2; Length 653;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10.5%; Score 330; DB 3; Length 653; 24.3%; Pred. No. 2.1e-12;
                Length 618;
                                                                                                                                                                                             Length 653;
                                                                                                                                                                                                                                                                                                                                                    Length 694;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 590;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 526;
                                                                                                                                                                                                                                                   AAB23033 standard; protein; 694 AA.
Human SLIT protein-like splice variant, SECX 3352358-1.
WO200053742-A2.
                                                                                                                                                                                                                                                                                                                                                                                                          AAB23034 standard; protein; 590 AA.
Human SLIT protein-like splice variant, SECX 3352358-2.
WO200053742-A2.
                                                                                                                                                                                         10.7%; Score 337; DB 6; 23.6%; Pred. No. 7.7e-13;
                                                                                                                                                                                                                                                                                                                                                  10.7%; Score 337; DB 3; 23.6%; Pred. No. 8.3e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 332; DB 4;
Pred. No. 1.2e-12;
                  10.7%; Score 337; DB 7; 27.2%; Pred. No. 7.2e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.6%; Score 333; DB 3; 25.8%; Pred. No. 1.2e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB24073 standard; protein; 653 AA.
Human PROll11 protein sequence SEQ ID NO:46.
WO200053755-A2.
14-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG04827 standard; protein; 526 AA. Novel human diagnostic protein #4818. WO200175067-A2.
                                                                      ADA23287 standard; protein; 653 AA.
Human SECX polypeptide, SEC5 #1.
US2003054514-AI.
20-MAR-2003.
(SHIM/) SHIMKETS R A.
(LARO/) LAROCHELLE W J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY28806 standard; protein; 653 AA.cc359 4 secreted protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY66694 standard; protein; 653 AA.
Membrane-bound protein PR01111.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU12390 standard; protein; 653 AA.
Human PRO1111 polypeptide sequence.
WO200140466-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   590 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADA23289 standard; protein; E
Human SECX polypeptide, SEC6.
US2003054514-Al.
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26.9%;
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                                                                                                                                                                                                                                                                                                          14-SEP-2000.
(CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-SEP-2000.
(CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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Best Local Similarity
RESULT 362
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PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity
RESULT 355
                                                                                                                                                                                                       Best Local Similarity
RESULT 356
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Best Local Similarity
RESULT 360
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(HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9963088-A2.
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Length 653;

Length 653;

RESULT 366

2382

Length 653;

Length 653;

Length 653;

RESULT 37:

BBBBBB

Length 653;

RESULT 364

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10.5%; Score 330; DB 6; Length 653; 24.3%; Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
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Novel human secreted and transmembrane protein PRO1111.
US2003022187-A1.
                                                    ABU72508 standard; protein; 653 AA.
Novel human secreted and transmembrane protein PRO1111.
US20303531.A1.
(22-747-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABUS9869 standard; protein; 653 AA.
Novel secreted and transmembrane protein PRO1111.
US2003017563-A1.
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22-43N-2003.
(GETH ) GENENTECH INC.
(GETH ) GENENTECH INC. 20.18; Score 330; DB 6;
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Human secreted/transmembrane protein (PRO) #219.
US2003036179-A1.
20-F88-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 10.5%; Score 330; DB 6; Best Local Similarity 24.3%; Pred. No. 2.1e-12; RESULT 376
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PA (GETH) GENENTECH INC.

Query Match

Best Local Similarity 24.3%; Pred. No. 2.1e-12;

RESULT 381
                                                                                                                                                        Score 330; DB 6;
Pred. No. 2.1e-12;
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                                                                                                                                                                                                                                                                               PA (GETH ) GENENTECH INC.
Query Match
10.5%; Score 330; DB 6;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 375
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Pred. No. 2.1e-12;
                                                                                                                                                                                                                                                                                                                                                                               AAO23105 standard; protein; 653 AA.
NAG14 'human modifier of p53 pathway' protein.
WO2003035833-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABUS8963 standard; protein; 653 AA.
Human sectreted/transmembrane protein, #93.
US2002142961-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human secreted/transmembrane protein, #93
US2003027162-Al.
06-FBB-2003.
                                                                                                                                                                                                                ABUG6788 standard; protein; 653 AA.
Human PRO polypeptide #219.
US2003036180-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABUS9257 standard; protein; 653 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABO25954 standard; protein; 653 AA
                                                                                                                                                      10.5%;
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24.3%;
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US2002127576-A1.
12-SEP-2002.
(GETH ) GENENTECH INC.
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(EXEL-) EXELIXIS INC.
FY Match
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              Best Local Similarity RESULT 373
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Best Local Similarity
RESULT 377
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Best Local Similarity
RESULT 380
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Best Local Similarity
RESULT 382
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  Query Match
                               Query Match 10.5%; Score 330; DB 4; Length 653; Best Local Similarity 24.3%; Pred. No. 2.1e-12;
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                                                                                                                                                                                                                                                                                                                                                                                   Score 330; DB 4; Length 653;
Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
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Novel human secreted and transmembrane protein PRO1111.
US2003032156-A1.
                                                                                                                                                                                                                                                                         AAB65217 standard; protein; 653 AA.

Human PRO1111 (UNQ554) protein sequence SEQ ID NO:229.
W0200073454-A1.
(GETH ) GENENTECH INC.
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Novel human secreted or transmembrane protein PRO1111.
US2002132252-A1.
                                                                                                                                                                                                                     10.5%; Score 330; DB 4; 24.3%; Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
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Human secreted/transmembrane protein PRO1111.
12-030320323-A1.
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Human secreted/transmembrane protein, #93.
US2002160384-A1.
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US2003027163-Al.
                                                                                         AAE09438 standard; protein; 653 AA. Human sbgPRO331a protein. W0200160850-A1. 23-AUG-2001. (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABU81088 standard; protein; 653 AA. Human PRO polypeptide #219. US2003004311.A1. G2-JAN-2003. (GETH ) GENENTECH INC.
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19-SEP-2002.
(GETH ) GENENTECH INC.
"G+Ch 10.5%;
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Best Local Similarity 24.3%;
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07-JUN-2001.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity
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Best Local Similarity
RESULT 369
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Best Local Similarity
RESULT 367
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Query

S D D E D

	RESULT 393  RESULT 393  RESULT 393  RESULT 394  DE AD019446 standard; protein; 653 AA.  DE NOVEL human secreted and transmembrane protein PRO1111.  PUS2003068796-A1.  PD 10-APR-2003.  PA (GETH) GRIENTECH INC.  QUETY Match  Best Local Similarity 24.3%; Pred. No. 2.1e-12;  RESULT 394  ID AD027987 standard; protein; 653 AA.  DE Human DOO nollocating #1916	PN US2003082704-AI. PN US2003082704-AI. PA (GETH ) GENENTECH INC. Query Match  Best Local Similarity 24.3%; Pred. No. 2.1e-12;  RESULT 39.5  ID ADA86466 standard; protein; 653 AA. DE Novel human secreted and transmembrane protein PRO1111.	Mes	ID ADA37740 standard; protein; 653 AA.  DE Human secreted/transmembrane protein PRO1111.  PD 109-JAN-2003.  PD 69-JAN-2003.  PA (GETH) GENENTECH INC.  Query Match  Best Local Similarity 24.3%; Pred. No. 2.1e-12;  RESULT 398  ID ADA47816 standard; protein; 653 AA.  DE Human PRO polypeptide #219.  PN 1022003073215-A1.	PA (GETH ) GENERATECH INC.  Query Match  Query Match  10.5%; Score 330; DB 6; Length 653;  Best Local Similarity 24.3%; Pred. No. 2.1e-12;  RESULT 399  ID ADA21426 standard; protein; 653 AA.  DE Human secreted/transmembrane polypeptide PRO1111.  PN US2003054404-A1.	Sur Sur Sur Ses
ID ABU59406 standard; protein; 653 AA.  DE Novel human secreted or transmembrane protein PR01344.  PN US2003027985-A1.  PD 06-FEB-2003.  10.5%; Score 330; DB 6; Length 653;  Best Local Similarity 24.3%; Pred. No. 2.1e-12;  RESULT 383  ID ABU67064 standard; protein; 653 AA.  DE Human secreted/transmembrane, PRO, protein SEQ ID 438.  PN US200303155-A1.	Suc Suc	BUI0878 standard; protein; 653 AA.  Janan PRO polypeptide #64.  52002123463-A1.  5-SEP-2002.  6-SEP-2002.  6-	NOVEL fluman secreted and transmembrane protein US2002177164-A1. 28-NOV-2002. (GETH ) GENENTECH INC. (GETH ) GENENTECH INC. 10.5%; Score 330; DB 6; Duery Match Local Similarity 24.3%; Pred. No. 2.1e-12; SULT 387 ABU88659 standard; protein; 653 AA. Human secreted and transmembrane polypeptide PR US2002197615-A1. 26-DEC-2002. (GETH ) GENENTECH INC. 10.5%; Score 330; DB 6;	SULT 388 SULT 388 ABO3403 standard; protein; 653 AA. Human PRO1111 polypeptide. US2003017981-A1. 23-GAN-2003. 10.5%; Score 330; DB 6; SULY 389 AD45957 standard; protein; 653 AA. Human secreted and transmembrane protein P	30-Jay 30-Jay 30-Jay (GETH (GETH Seer Loc SULT 390 ADA76 Human	PA (GETH ) GENENTECH INC.  PA (GETH ) GENENTECH INC.  Query Match 10.5%; Score 330; DB 6; Length 653;  Best Local Similarity 24.3%; Pred. No. 2.1e-12;  RESULT 391  ID ADA19038 standard; protein; 653 AA.  DE Human PRO polypeptide #219.  PN US2003054517-A1.  PD 20-MAR-2003.

US2003082694-A1.

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Length 653;
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                                                                                                                                                                                                                                                 ADA85914 standard; protein; 653 AA.
Novel human secreted and transmembrane protein FRO1111.
US2003082693-A1.
01-MAY-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADA87569 standard; protein; 653 AA.
Novel human secreted and transmembrane protein PRO1111 US2003087345-A1.
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Novel human secreted and transmembrane protein PRO1111
                                                                        Query Match 10.5%; Score 330; DB 6;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 402
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Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
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Human secreted/transmembrane protein PRO1111.
US2003054359-A1.
20-MAR-2003.
            ADA67611 standard; protein; 653 AA.
Human PRO polypeptide #219.
US2003068795-A1.
                                                                                                                             ADB30618 standard; protein; 653 AA.
Human PRO polypeptide #219.
US2003068794-A1.
                                                                                                                                                                                                                                                                                                                                                                      ADA17757 standard; protein; 653 AA.
Human PRO1111 polypeptide.
US2003054987-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADA97126 standard, protein; 653 AA.
Human PRO polypeptide #219.
N US2003082705-A1.
O1-MAY-2003.
A (GETH ) GENENTECH INC.
OUERY MATCh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADA79430 standard; protein; 653 AA.
Human PRO polypeptide #219.
US2003082763-Al.
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08-Mav-^^-
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24.3%;
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24.3%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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RESULT 406
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RESULT 407
RESULT 401
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Score 330; DB 6; Length 653;
Pred. No. 2.1e-12;
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Novel human secreted and transmembrane protein PRO1111.
US200344945-A1.
UG-MAA-2003.
(GETAR - 10 GENENTECH INC.
10.5%; Score 330; DB 6; Length
st Local Similarity 24.3%; Pred. No. 2.1e-12;
                                                                                                                                                                                                          ADBIE887 standard; protein; 653 AA.
Novel human secreted and transmembrane protein PRO1111.
US2003073211-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADB19998 standard; protein; 653 AA.
Novel human secreted and transmembrane protein PRO1111.
US2003082691-A1.
                                                                                                                                                               Score 330; DB 6;
Pred. No. 2.1e-12;
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(GETH ) GENENTECH INC.

(GETH ) GENENTECH INC.

10.5%; Score 330; DB 6;

Lery Match
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Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
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Human secreted/transmembrane protein PRO1111.
US2003059832-A1.
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Human PRO polypeptide SEQ ID NO 438.
US2003077713-A1.
                                                                                                                                                                                                                                                                                                                                  Human PRO polypeptide #219.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human PRO polypeptide #219. 01-Mav-2-2
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                                                                               653 AA
                                                                                                                                                                                                                                                                                                                                                                           US200sv...
24-APR-2003.
(GETH ) GENENTECH INC.
4srch 10.5%; S
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01-MAY-2003.
(GETH ) GENENTECH INC.
10.5%;
                       Best Local Similarity 24.3%;
RESULT 411
ID ADB14926 standard; protein. 6
DE Human pool
                                                                                                                                                        Best Local Similarity 24.3%;
RESULT 412
                                                                                                                                                                                                                                                                                           10.5%;
                                                                            ADB14926 standard; protein;
Human PRO polypeptide #219.
US2003087351-A1.
08-MAY-2003.
(GETH ) GENENTECH INC.
01-MAY-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                             17-APR-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-APR-2003.
(GETH ) GENENTECH INC.
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RESULT 418
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
RESULT 414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity RESULT 417
                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                             RESULT 413
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24.3%; Pred. No. 2.1e-12;

24

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ADA47061 standard; protein; 653 AA.
Human PRO polypeptide #219.
US2003073210-A1.
17-APR-2003.
(GETH ) GENENTECH INC.
10.5%; Score 330; DB 6; Length 653;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.5%; Score 330; DB 6; Length 653; 24.3%; Pred. No. 2.1e-12;
                                                                                                                                           Score 330; DB 6; Length 653; Pred. No. 2.1e-12;
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                Length 653;
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                                                                                                                                                                                                                                                                                                                          ADA85362 standard; protein; 653 AA.
Novel human secreted and transmembrane protein PRO1111
US2003082695-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADA84810 standard; protein; 653 AA.

Novel human secreted and transmembrane protein PRO1111
US2003082708-A1.
                Score 330; DB 6;
Pred. No. 2.1e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 330; DB 6;
Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
                                                                                                                                                                                                                                                                           10.5%; Score 330; DB 6; 24.3%; Pred. No. 2.1e-12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADA38670 standard; protein; 653 AA.
Human secreted/transmembrane protein PRO1111.
US2003059780-A1.
                                                              ADA82321 standard; protein; 653 AA.
Human PRO polypeptide #219.
US2003082701-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADA80594 standard; protein; 653 AA.
Human PRO polypeptide #219.
US200308271-A1.
01-MAY-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                             protein; 653 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         653 AA
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01-MAY-2003.
(GETH ) GENENTECH INC.
AACCh ... 12 10 5%;
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               10.5%;
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US2003082703-A1.
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US2003073216-A1.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                         17-APR-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
(GETH ) GENENTECH INC
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Best Local Similarity
RESULT 425
ID ADA80594 standard; pr
DE Human PRO polypeptide
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC
                                                                                                                                                          Best Local Similarity RESULT 421
                         Best Local Similarity
RESULT 420
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Best Local Similarity
RESULT 427
                                                                                                                                                                                            ADA75284 standard;
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                Query Match
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ID ADB3000
DE Human I
PN US20030
PD 17-APR
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Length 653;
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15-MAY-2003.

(GETY Match 10.5%; Score 330; DB 6; 10.5% S
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Human PRO polypeptide #219.
US2003096386-A1.
22-MAY-2003.
(GETH ) GENENTECH INC.
10.5%; Score 330; DB 6; Et Local Similarity 24.3%; Pred. No. 2.1e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 330; DB 6;
Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
                                                                                                                                                                                                                        Score 330; DB 6;
Pred. No. 2.1e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 330; DB 6;
Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADA92791 standard; protein; 653 AA.
Human secreted/transmembrane protein PRO1111.
US2003060407-A1.
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                                             Human PRO polypeptide SEQ ID NO 438 (0S200307715-Al.
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Human PRO polypeptide #219.
US2003077721-A1.
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24-APR-2003.
(GETH ) GENENTECH INC.
10.5%; St.
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24.3%;
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Best Local Similarity 24.3%;
                                                                                                                                              PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%;
Best Local Similarity 24.3%;
RESULT 430
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Human PRO polypeptide #219.
US2003082690-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 438
Best Local Similarity RESULT 429
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Best Local Similarity
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RESULT 431
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US2003049817-A1.
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(GETH ) GEN
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RESULT 434
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Human PRO polypeptide #219
                                                                                        Length 653;
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Pred. No. 2.1e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 330; DB 7; Length 653;
Pred. No. 2.1e-12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 653
                                                                                                                                                                                                                                                                          ADB21816 standard; protein; 653 AA.
Novel human secreted and transmembrane protein PRO1111.
US2003082765-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADA88121 standard; protein; 653 AA.
Novel human secreted and transmembrane protein PRO1111.
US2003082700-A1.
01-MAY-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADA46509 standard; protein; 653 AA.
Novel human secreted and transmembrane protein PRO1111.
US2003054516-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADAB7018 standard; protein; 653 AA.
Novel human secreted and transmembrane protein PRO1111
US2003082709-A1.
                                                                                     Score 330; DB 6;
Pred. No. 2.1e-12;
                                                                                                                                                                                                                          10.5%; Score 330; DB 6; 24.3%; Pred. No. 2.1e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 330; DB 7;
Pred. No. 2.1e-12;
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ADA96022 standard; protein; 653 AA.
Human PRO polypeptide #219.
US2003082759-A1.
                                                                                                                                   ADB26331 standard; protein; 653 AA.
Human PRO polypeptide #219.
US2003082760-A1.
                                                                                                                                                                                                                                                                                                                                                                                                              ADA77595 standard; protein; 653 AA. Human PRO polypeptide #219. US2003068797-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADB18335 standard; protein; 653 AA, Human PRO polypeptide #219.
US2003077710-A1.
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Human PRO polypeptide #219.
US2003082699-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADB29091 standard; protein; 653 AA
                                                                              Best Local Similarity 24.3%;
RESULT 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.5%;
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RESULT 447
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Best Local Similarity 24.3%;
                                                01-MAY-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-APR-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                                                                                                                                         (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                              (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
RESULT 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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ID ADA7759
DE Human E
PN US20030
PD 10-APR-
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RESULT 443
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RESULT 444
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Score 330; DB 7; Length 653;
Pred. No. 2.1e-12;
                                                                                                                                                                         10.5%; Score 330; DB 7; Length 653; 24.3%; Pred. No. 2.1e-12;
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Novel human secreted and transmembrane protein PRO1111.
US2003073213-A1.
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Novel human secreted and transmembrane protein PRO1111.
US2003087344-A1.
                                                                                                                                                                                                                                                                                                                                                                   ADA22352 standard; protein; 653 AA.
Human secreted/transmembrane polypeptide PRO1111.
VS2003040473-A1.
27-FBB-2003.
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ID ADA06518 standard; protein; 653 AA.

DE Human secreted/transmembrane PRO polypeptide #64.

PN US2003049638-A1.

PD 13-MAR-2003.

Query Match

Best Local Similarity 24.3%; Pred. No. 2.1e-12; RESULT 457
                                                                                                                                                                                                                                                                                                                    Score 330; DB 7;
Pred. No. 2.1e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                          10.5%; Score 330; DB 7; 24.3%; Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
                                                                                                ABO51169 standard; protein; 653 AA.
Human secreted/transmembrane protein PRO1111
US2003044806-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABO22539 standard; protein; 653 AA.
Human secreted/transmembrane protein PRO1111.
US2003017982-A1.
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US2003022239-Al.
30-DAN-2003.
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                                                                                                                                                                                                                        ADA77043 standard; protein; 653 AA.
Human PRO polypeptide #219.
US2003059909-A1.
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17-APR-2003.
(GETH ) GENENTECH INC.
10.5%; S'
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24.3%;
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PA (GETH ) GENENTECH INC.

Query Match 10.5%;

Best Local Similarity 24.3%;

RESULT 45.3

ID ADB27435 standard; protein; 6
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24.3%;
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24.3%;
                                                                                                                                                                                                                                                                             27-MAR-2003.
(GETH ) GENENTECH INC.
US2003082706-A1.
01-MAY-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
RESULT 450
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Best Local Similarity
RESULT 452
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RESULT 448
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Best Local Similarity
RESULT 451
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RESULT 454
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RESULT 455
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Length 653;

us-09-943-780-69.ragspdi

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10.5%; Score 330; DB 7; Length 653; 24.3%; Pred. No. 2.1e-12;
 01-MAY-2003.
(GETH) GENENTECH INC.
ETY MATCh 10.5%; Score 330; DB 7; Length 653;
st Local Similarity 24.3%; Pred. No. 2.1e-12;
                                                                                                                                                                                                                                                                                                                                                                       ADB39563 standard; protein; 653 AA.
Novel human secreted and transmembrane protein PRO1111.
01-MAY-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADB47186 standard; protein; 653 AA.
Novel human secreted and transmembrane protein PRO1111
US2003082687-A1.
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Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
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Pred. No. 2.1e-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADB34555 standard; protein; 653 AA. Human PRO polypeptide SEQ ID NO 438 US2003077717-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADB35659 standard; protein; 653 AA.
Human PRO polypeptide SEQ ID NO 438
US2003077719-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADB86793 standard, protein; 653 AA. Human PRO polypeptide #219. US2003002697-A1. 01-MAY-2003. (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                    ADB90462 standard; protein; 653 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein; 653 AA
                                                                                        protein; 653 AA
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01-MAY-2003.
(GETH ) GENENTECH INC.
wetch 10.5%; S
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24.3%;
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PA (GETH ) GENENTECH INC.
Query Match 10.5%;
Best Local Similarity 24.3%;
RESULT 469
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Best Local Similarity 24.3%;
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Local Similarity 24.3%;
                                                                                      ADB89730 standard; protein;
Human PRO polypeptide #219.
US2003082698-A1.
01-MAY-2003.
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US2003082762-A1.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity
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Best Local Similarity
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RESULT 472
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                                                                         RESULT 467
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                                                                                                                                                                                                                   Length 653;
                                                                         Length 653;
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Pred. No. 2.1e-12;
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Novel human secreted and transmembrane protein PRO1111.
US2003082689-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADB38178 standard; protein; 653 AA.
Novel human secreted and transmembrane protein PRO1111.
US2003087347-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADB38730 standard; protein; 653 AA.
Novel human secreted and transmembrane protein PRO1111
US2003082766-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADA92415 standard; protein; 653 AA.

Novel human secreted and transmembrane protein PRO1111
US2003082712-A1.
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Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
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                                                                       Score 330; DB 7;
Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
ADA39211 standard; protein; 653 AA.
Human secreted/transmembrane protein PRO1111
US2003059782-A1.
                                                                                                                                                                                                                                                                                                                                                                                                              ADB23693 standard; protein; 653 AA.
Human PRO polypeptide SEQ ID NO 438.
US2003077712-A1.
                                                                                                                                                                                                                                                                   ADB22920 standard; protein; 653 AA.
Human PRO polypeptide #219.
US2003077711-A1.
24-APR-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADB96237 standard; protein; 653 AA. Human PRO polypeptide #64. US2003054403-A1. 20-MAR-2003.
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Human PRO polypeptide #219.
US2003087352-A1.
                                                                                                                           ADA67059 standard, protein, 653 AA.
Human PRO polypeptide #219.
US2003068793-A1.
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08-MAY-2003.
(GETH ) GENENTECH INC.
Match 'larity 24.3%;
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24.3%;
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24.3%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                                                                                                                10-APR-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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RESULT 461
ID ADA92415 standard; pi
DE Novel human secreted
PD US2003082712-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC
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RESULT 464
ID ADB96337 standard; p
DE Human PRO polypeptid
PN US2003054403-A1.
PD 20-MAR-2003.
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ID ADB3114
BE NOVEL HUMAN SECRETE PN US2003087347-A1.
PD 08-MAY-2003
PA (GETH ) GENENTECH IN
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Best Local Similarity
RESULT 460
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Best Local Similarity
RESULT 463
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                                                                                        Best Local Similarity RESULT 458
                                                                                                                                                                                                                   Query Match
Best Local Similarity
RESULT 459
                                                          27-MAR-2003.
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Length 653;

Length 653;

A D D E D

Length 653;

Length 653;

Length 653;

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Best Local Similarity RESULT 488
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RESULT 494
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                   Length 653;
                                                                                                                                                 10.5%; Score 330; DB 7; Length 653; 24.3%; Pred. No. 2.1e-12;
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Beet Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 479
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Pred. No. 2.1e-12;
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                                                                                                                                                                                                                                                                                    10.5%; Score 330; DB 7; Length 653; 24.3%; Pred. No. 2.1e-12;
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                                                                                                                                                                                                                                                                                                                            ADB46606 standard; protein; 653 AA.
Novel human secreted and transmembrane protein PRO1111.
US2003082692-A1.
01-MAY-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADC50479 standard, protein, 653 AA.
Novel human secreted and transmembrane protein PROll11.
US2003092106-A1.
                 Score 330; DB 7;
Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
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Human secreted/transmembrane protein PRO1111.
13-MAR-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADC07417 standard; protein; 653 AA.
Human secreted/transmembrane protein PRO1111.
US2003068647-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human secreted/transmembrane protein PRO1111. US200059403-A1.
                                                         ADB35107 standard; protein; 653 AA.
Human PRO polypeptide SEQ ID NO 438
US2003077718-A1.
                                                                                                                                                                                        Human PRO polypeptide SEQ ID NO 438.
US2003077720-Al.
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US2003064375-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADC57709 standard; protein; 653 AA. Human PRO polypeptide #64. US2003027754-Al. 06-FEB-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADC55073 standard, protein, 653 AA.
Human PRO polypeptide #64.
US2003045463-Al.
06-MAR-2003.
                 10.5%;
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24.3%;
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24.3%;
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24.3%;
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(GETH ) GENENTECH INC.
(GETH ) GENENTECH INC.
                                                                                                                  24-APR-2003.
(GETH ) GENENTECH INC
                                                                                                                                                               Best Local Similarity RESULT 477
                                                                                                                                                                                                                                                                                                   Local Similarity
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Best Local Similarity
RESULT 480
               Query Match
Best Local Similarity
RESULT 476
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Best Local Similarity
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RESULT 484
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Best Local S
RESULT 485
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RESULT 478
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A D S G D

2 2 E C

A D D E D

Best RESULT

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Length 653;
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Novel human secreted and transmembrane protein Seg ID438.
US2003087364-A1.
08-MAY-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADC57366 standard; protein; 653 AA.
Novel human secreted and transmembrane protein Seg ID438.
US2003087366-A1.
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Novel human secreted and transmembrane protein Seg ID438.
US2003087363-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human secreted and transmembrane protein Seq ID438 US2003087365-A1.
                                                                                                                                                                                                                                                                                ADC60005 standard; protein; 653 AA.
Novel human secreted and transmembrane protein PROIII1.
US2003092105-A1.
15-MAY-2003.
(GETH) GENENTECH INC.
10.5%; Score 330; DB 7; Length
EL Local Similarity 24.3%; Pred. No. 2.1e-12;
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Novel human secreted and transmembrane protein PRO1111.
US2003087367-A1.
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Novel human secreted and transmembrane protein PRO1111.
US2003087361-A1.
08-MAY-2003.
(GETH ) GENENTECH INC.
                                                                                                  ACT2026 standard; protein; 653 AA.
Novel human secreted and transmembrane protein PRO1111
US2003092107-A1.
15-MAY-2003
(GETH ) GENENTECH INC.
PA (GETH ) GENENTECH INC.

Query Match
Best Local Similarity 24.3%; Fred. No. 2.1e-12;

RESULT 486
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PA (GETH) GENENTECH INC.

Query Match

Best Local Similarity 24.3%; Pred. No. 2.1e-12;

RESULT 489
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                                                                                                                                                                                                                  Score 330; DB 7;
Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADC53012 standard; protein; 653 AA.
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PA (GETH ) GENENTECH INC.
Query March
Best Local Similarity 24.3%;
RESULT 490
                                                                                                                                                                                                                Query Match 10.5%;
Best Local Similarity 24.3%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Length 653; ADC80623 standard; protein; 653 AA. Novel human secreted and transmembrane protein PRO1111 US2003092103-A1. Novel human secreted and transmembrane protein PRO1111. US2003073090-A1. ADC80071 standard; protein; 653 AA.
Novel human secreted and transmembrane protein PRO1111.
US2003087358-A1. Novel human secreted and transmembrane protein PRO1111 US2003087354-A1. ADD07528 standard; protein; 653 AA. Novel human secreted and transmembrane protein PRO1111 Score 330; DB 7; Pred. No. 2.1e-12; 10.5%; Score 330; DB 7; 24.3%; Pred. No. 2.1e-12; 10.5%; Score 330; DB 7; 24.3%; Pred. No. 2.1e-12; ADC48563 standard; protein; 653 AA. Human PRO polypeptide #219. US2003194773-A1. Human PRO polypeptide #219. US2003194776-A1. ADDI1130 standard; protein; 653 AA. Human PRO polypeptide #219. US2003194774-A1. RESULT 511
ID ADC48011 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US200319471-A1. protein; 653 AA protein; 653 AA 10.5%; 24.3%; 10.5%; 24.3%; 10.5%; Best Local Similarity 24.3%; RESULT 506 y Match Local Similarity 24.3%; Query Match 10.5%; Best Local Similarity 24.3%; RESULT 510 Query Match 10.5%; Best Local Similarity 24.3%; 24.3%; Human PRO polypeptide #64. US2003059833-A1. 16-OCT-2003. (GETH ) GENENTECH INC. US2002193299-A1. 19-DEC-2002. (GETH ) GENENTECH INC. (GETH ) GENENTECH INC. 15-MAY-2003. (GETH ) GENENTECH INC. 16-OCT-2003. (GETH ) GENENTECH INC. 16-OCT-2003. (GETH ) GENENTECH INC. 16-OCT-2003. (GETH ) GENENTECH INC. Best Local Similarity Best Local Similarity RESULT 512 Best Local Similarity RESULT 513 Best Local Similarity RESULT 505 ID ADD10092 standard; ADD04667 standard; ADC82419 standard; Best Local Similarity RESULT 509 27-MAR-2003. Query Match Query Match Query Match Query Match Query Match Query Match Best RESULT

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RESULT 523
ID ADD51840
                                                                                                                                                             vuery Match 10.5%; Score 330; DB 7; Length 653; Beet Local Similarity 24.3%; Pred. No. 2.1e-12; RESULT 515
                                 Query Match 10.5%; Score 330; DB 7; Length 653; Best Local Similarity 24.3%; Pred. No. 2.1e-12;
                                                                                                                                                                                                                                                                                                                  Score 330; DB 7; Length 653; Pred. No. 2.1e-12;
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Novel human secreted and transmembrane protein PRO1111.
US2003203438-A1.
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                                                                                  ADD06848 standard; protein; 653 AA.
Novel human secreted and transmembrane protein PRO1111 US2002193300-A1.
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Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
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182003194775-Al.
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Human PRO polypeptide #219.
US2003194769-A1.
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Human PRO polypeptide #219.
US2003194792-A1.
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Human PRO polypeptide #64.
US2003077593-A1.
24-APR-2003.
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Human PRO polypeptide #64.
24-0303077594-Al.
24-APR-2003.
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24.3%;
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PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity 24.3%;
RESULT 519
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Best Local Similarity 24.3%;
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Best Local Similarity 24.3%;
RESULT 518
                                                                                                                                                                                                                                                                                   16-OCT-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                                                                      19-DEC-2002.
(GETH ) GENENTECH INC.
08-MAY-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
RESULT 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity RESULT 520
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Query Match 10.5%; Score 330; DB 7; Length 653; Best Local Similarity 24.3%; Pred. No. 2.1e-12; RESULT 529
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                                                                                              Score 330; DB 7; Length 653;
Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    ID ADD54255 standard; protein; 653 AA.

DE Novel human secreted and transmembrane protein PRO1111.

PN US203203432-A1.

PD 30-CCT-2003.

PA (GETH) GENEWIECH INC.

Query Match 10.5%; Score 330; DB 7; Length Best Local Similarity 24.3%; Pred. No. 2.1e-12;
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Novel human secreted and transmembrane protein PRO1111.
US2003087304-A1.
08-MAY-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                      10.5%; Score 330; DB 7; 24.3%; Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
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DE Human PRO polypeptide #219.

PN US2003199055-A1.

PA (GETH ) GENENTECH INC.

Query Match

Best Local Similarity 24.3%; Pred. NO RESULT 530
ADD51840 standard; protein; 653 AA. Human PRO polypeptide #219. US2003194779-Al. 16-OCT-2003. (GETH ) GENENTECH INC. 10-5%; Score 33 Dery Match 24.3%; Pred. NG Set Local Similarity 24.3%; Pred. NG
                                                                                                       Best Local Similarity 24.3%; Score RESULT 524
ID ADD02619 standard; protein; 653 AA. PN US2003203431-A1.
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(052003199057-A1.
                                                                                                                                                                                                                                                                                                                 ADD02073 standard; protein; 653 AA. Human PRO polypeptide #219. US2003203430-A1. 30-OCT-2003. (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADD54598 standard, protein, 653 AA Human PRO polypeptide #64. UG2002132253-A1. 19-SEP-2002. (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADE32379 standard; protein; 653 AA.
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Human PRO polypeptide #219.
US2003199030-Al.
23-OCT-2003.
(GET) GENENTECH INC.
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23-007-2003.
(GETH ) GENENTECH INC.
10.5%;
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Best Local Similarity 24.3%;
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RESULT 525
                                                                                                                                                                                                                                        (GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 531
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RESULT 526
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                                                                                                Query Match
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Score 330; DB 7; Length 653;
Pred. No. 2.1e-12;
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Novel human secreted and transmembrane protein PRO1111
US2003087305-A1.
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Novel human secreted and transmembrane protein PRO1111 US2003194766-A1.
                                           Score 330; DB 7;
Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
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Pred. No. 2.1e-12
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Human PRO polypeptide #219.
US2003203429-A1.
                                                                                                                                                                                                                 ADE18992 standard, protein, 653 AA.
Human PRO polypeptide #219.
US2003199026-A1.
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Human PRO polypeptide #219.
US2003199032-A1.
23-OCT-2003.
                                                                                           protein; 653 AA.
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24.3%;
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PA (GETH ) GENENTECH INC.
Query Match 10.5%;
Best Local Similarity 24.3%;
RESULT 547
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Local Similarity 24.3%;
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Human PRO polypeptide #219.
US2003199033-A1.
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                                                                                                          Human PRO polypeptide #219.
US2003199025-A1.
23-OCT-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
              16-OCT-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC
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Best Local Similarity
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                                                                                                                                                                                    Local Similarity
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ADD95977 standard;
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Best Local Similarity
RESULT 549
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                                                        Best Local Similarity RESULT 542
                                                                                           ADE19544 standard;
 US2003194768-A1.
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RESULT 544
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RESULT
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Pred. No. 2.1e-12;
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Novel human secreted and transmembrane protein PRO1111.
US2003194791-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADE31483 standard; protein; 653 AA.
Novel human secreted and transmembrane protein PRO1111
US2003194767-A1.
Novel human secreted and transmembrane protein PRO1111
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1 (GETH ) GENENTECH INC.

10.5%; Score 330; DB 7;

Query Match 10.5%; Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
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US2003199023-A1.
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US2003207417-Al.
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                                                                                                                                                                                                                                                                                                                     Best Local Similarity 24.3%; pred.
RESULT 535
ID ADE42071 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
                                                                                                        ADE22311 standard; protein; 653 AA.
Human PRO polypeptide #219.
US2003199056-A1.
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Human PRO polypeptide #219.
US2003199053-A1.
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Human PRO polypeptide #219.
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23-OCT-2003.
(GETH ) GENENTECH INC.
Warch 10.5%; Sr
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23-007-2003.
(GETH ) GENENTECH INC.
Match 138;
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24.3%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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              US2003194765-A1.
16-OCT-2003.
(GETH ) GENENTECH INC.
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A ) GENENTECH 1

Best Local Similarity A

RESULT 540
ID ADD80087 stand>
DE Human PRO F

PN US2003>
PD 06-Y
                                                                     Best Local Similarity
RESULT 533
ID ADE22311 standard; pr
DE Human PRO polypeptide
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC
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Best Local Similarity
RESULT 536
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Best Local Similarity
RESULT 538
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Best Local Si
RESULT 534
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RESULT 539
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Length 653;

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Score 330; DB 7; Length 653;
Pred. No. 2.1e-12;
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Novel human secreted and transmembrane protein PRO1111.
US2003207386-A1.
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Novel human secreted and transmembrane protein PRO1111
US2003207381-A1.
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Novel human secreted and transmembrane protein PRO1111 US2003207379-A1.
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Novel human secreted and transmembrane protein PRO1111
US2003207385-A1.
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Novel human secreted and transmembrane protein PRO1111
US2003207387-A1.
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Novel human secreted and transmembrane protein PRO1111.
US2003203388-A1.
 10.5%; Score 330; DB 7; 24.3%; Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
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Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 565
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Pred. No. 2.1e-12;
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(GETH ) GENENTECH INC.
(GETH ) GENENTECH INC.
(ery Match 10.5%; Score 330; DB 7;
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Pred. No. 2.1e-12
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Pred. No. 2.1e-12;
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Human PRO polypeptide #219.
US2003207372-A1.
                                                           protein; 653 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AD135410 standard; protein; 653 AA. Human PRO polypeptide #64. US2003050457-Al. 13-MAR-2003.
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06-NOV-2003.
(GETH ) GENENTECH INC.
10.5%;
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PA (CETH) GENENTECH INC.
Query Match 10.5%;
Best Local Similarity 24.3%;
                                                   ADG80628 standard; protein; (Human PRO polypeptide #219. US200320733-Al. 06-NOV-2003. (GETH ) GENENTECH INC.
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PA (GETH ) GENENTECH INC.

QUENTY MARCh 10.5%;

Best Local Similarity 24.3%;

RESULT 568
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Query GETH ) GENENTECH INC.

Query Match 10.5%;

Best Local Similarity 24.3%;
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(GETH ) GENENTECH INC.
             Best Local Similarity RESULT 560
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RESULT 566
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Best Local Similarity
RESULT 567
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Novel human secreted and transmembrane protein PRO1111
US2003207355-A1.
06-NOV-2003.
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Novel human secreted and transmembrane protein PRO1111 US2003207384-A1.
                   Score 330; DB 7;
Pred. No. 2.1e-12;
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Human PRO1111 amino acid sequence SEQ ID NO:229.
US2002199148 Al.
26-DEC-2002.
(GETH ) GENENTECH INC.
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Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
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(GETH ) GENENTECH INC.
(GETH ) GENENTECH INC.
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(GETH ) Generaty 24.3%; Pred. No. 2.1e-12;
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US2003194777-A1.
                                                                       ADD80639 standard; protein; 653 AA.
Human PRO polypeptide #219.
US2003207418-Al.
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US2003199028-A1.
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US2003199031-Al.
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Human PRO polypeptide #219.
US2003199034-A1.
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Human PRO polypeptide #219.
US2003207370-A1.
                 10.5%;
24.3%;
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Best Local Similarity 24.3%;
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RESULT 554
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 556
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RESULT 558
                               Best Local Similarity RESULT 551
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Length 653;

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Best RESULT

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Length 653

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Best Local Similarity 24.3%; Score 330; DB 8; Length 653; RESULT 578
ID ADD87987 creater.
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                                                                               Length
              ADH99902 standard; protein; 653 AA.
Novel human secreted and transmembrane protein PRO1111.
US2003049682-A1.
                                                                                                                                                                                                                                                   ADM82618 standard; protein; 653 AA.
Novel human secreted and transmembrane protein PRO1111.
US2003087135-A1.
(G8-MAY-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                   אא. Standard; protein; 653 AA.
Novel human secreted and transmembrane protein PROllll.
US200308733-A1.
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Novel human secreted and transmembrane protein PRO1111
US2003087385-A1.
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Novel human secreted and transmembrane protein PRO1111.
US2003087356-A1.
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Novel human secreted and transmembrane protein PRO1111.
US2003087357-A1.
08-MAY-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADC81175 standard; protein; 653 AA.
Novel human secreted and transmembrane protein PRO1111
US2003092115-A1.
                                                                                                                        ADH81449 standard; protein; 653 AA.
Novel human secreted and transmembrane protein PRO1111
US2003207377-A1.
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(GETH ) GENENTECH INC.
iry Match 10.5%; Score 330; DB 7;
iry Match 24.3%; Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
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Pred. No. 2.1e-12
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Pred. No. 2.1e-12
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Human PRO polypeptide #219.
US2003100087-A1.
29-MAY-2003.
(GETH ) GENENTECH INC.
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08-MAY-2003.
(GETH ) GENENTECH INC.
Watch 10.5%; Sr
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08-MAY-2003.
(GETH ) GENENTECH INC.
Match 'larity 24.3%;
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24.3%;
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(GETH ) GENENTECH INC.
                                                                                                                                                                      06-NOV-2003.
(GETH ) GENENTECH INC.
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RESULT 576
ID ADC81175 standard; pr
DE Novel human secreted
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
RESULT 575
ID ADN14913 standard; pi
DE Novel human secreted
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
RESULT 573
ID ADN16646 standard, p.
DE Novel human secreted
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH IN
                                                                                                                                                                                                                  Best Local Similarity
RESULT 571
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Best Local Similarity
RESULT 577
                                                                               Query Match
Best Local Similarity
RESULT 570
                                                            13-MAR-2003.
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RESULT 569
ID ADH999
DE Novel
PN US2003
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Score 330; DB 8; Length 653; Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
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                                                             Score 330; DB 8;
Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
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US2003092110-A1.
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Human PRO polypeptide #219.
US2003194794-A1.
                                                                                                         ADD86391 standard; protein; 653 AA. Human PRO polypeptide #219. US2003203440-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADE24610 standard; protein; 653 AA. Human PRO polypeptide #219. US2003092111-A1.
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Human PRO polypeptide #219.
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15-MAY-2003.
(GETH ) GENENTECH INC.
"..rch 10.5%; S
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24.3%;
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Local Similarity 24.3%;
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Best Local Similarity 24.3%;
RESULT 583
                                                                                                                                                                                                                                ADE75839 standard; protein;
Human PRO polypeptide #219.
US2003211571.A1.
(3ETH ) GENENTECH INC.
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Best Local Similarity 24.3%;
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Human PRO polypeptide #219.
US2003203439-A1.
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RESULT 585
ID ADEB9301 standard; protein;
DB Human PRO polypeptide #219.
PN US2003199062-Al.
Human PRO polypeptide #219.
US2003092113-A1.
15-MAY-2003.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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                                               (GETH ) GENENTECH INC
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                                                                          Best Local Similarity RESULT 579
                                                                                                                                                                                                                                                                                                                                            RESULT 581
ID ADE23415 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
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(GETH ) GENENTECH INC.
                                                                                                    Length 653;
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Novel human secreted and transmembrane protein PRO1111.
US2003199051-A1.
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Novel human secreted and transmembrane protein PRO1111.
US2003199058-A1.
23-OCT-2003.
               US400-1--
23-OCT-2003.
(GFH) GENENTECH INC.
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Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
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                                                                                                                                                                                                                                                                                                                                                                                                                        ADE91180 standard; protein; 653 AA. Human PRO polypeptide #219.
US2003199061-A1.
23-OCT-2003.
(GETH ) GENENTECH INC.
20ery Match
10.5%; Score 33
                                                                                                                                                                   Human PRO polypeptide #219.
US2003199027-Al.
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Human PRO polypeptide #219.
USZ003199052-AA.
23-OCT-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADF35355 standard; protein; 653 AA.
Human PRO1111 polypeptide.
US2003194760-A1.
16-OCT-2003.
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Human PRO polypeptide #219.
US2003199060-A1.
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Human PRO polypeptide #219.
US2003199029-A1.
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Human PRO polypeptide #219.
US2003199063-A1.
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23-OCT-2003.
PA (GETH) GENENTECH INC.
QUERY MATCh
Best Local Similarity 24.3%; Pre
RESULT 589
ID ADE91180 standard; proton
PR US20031990f**
PA 23-OC**
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Query Match
Best Local Similarity 2.
RESULT 591
ID ADE95321 stander
DE Human PRO receive PN US20031.
PN US20031.
PA
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                           Query Match
Best Local Similarity
RESULT 588
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Best Local Similarity
RESULT 590
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RESULT 595
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US2003199054-A1.
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Query Match 10.5%; Score 330; DB 8; Length 653; Best Local Similarity 24.3%; Pred. No. 2.1e-12; RESULT 600
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PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.5%; Score 330; DB 8; Length 653; 24.3%; Pred. No. 2.1e-12;
  Length 653
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                                                                                                                                                                                                                                                                                                                                                           MGG22140 standard; protein; 653 AA.
Novel human secreted and transmembrane protein PRO1111 US2003207360-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADG24333 standard; protein; 653 AA.
Novel human secreted and transmembrane protein PRO1111
US2003207426-A1.
  Score 330; DB 8;
Pred. No. 2.1e-12;
                                                                                                                                                        Score 330; DB 8;
Pred. No. 2.1e-12;
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PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8;
Best Local Similarity 24.3%; Fred. No. 2.1e-12;
RESULT 603
                                                                                                                                                                                                                                                                                                             Score 330; DB 8;
Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
                                                      ADG11605 standard; protein; 653 AA.
Human PRO1111 polypeptide.
US2003228655-A1.
                                                                                                                                                                                                           ADG02354 standard; protein; 653 AA.
Human PRO polypeptide #219.
US2003207352-A1.
G6-NOV-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human PRO polypeptide #219.
05-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADG20210 standard; protein; 653 AA. Human PRO polypeptide #219. US2003207376-A1. G6-NOV-2003. (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADF98687 standard; protein; 653 AA.
Human PRO polypeptide #219.
US2003208055-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADF99239 standard; protein; 653 AA. Human PRO polypeptide #219. US2003207353-A1. G6-NOV-2003. (GETH ) GENENTECH INC.
10.5%;
24.3%;
                                                                                                            11-DEC-2003.
(GETH ) GENENTECH INC.
ery Match 10.5%;
st_Local Similarity 24.3%;
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06-NOV-2003.
(GETH ) GENENTECH INC.
Match '17-rity 24.3%;
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Best Local Similarity 24.3%;
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(GETH ) GENENTECH INC.
              Best Local Similarity RESULT 597
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Best Local Similarity
RESULT 602
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RESULT 605
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RESULT 598
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Score 330; DB 8; Pred. No. 2.1e-12;

Length 653;

Query Match

Query Match

Length 653;

Score 330; DB 8; Pred. No. 2.1e-12;

Length 653;

Length 653;

Length 653;

Score 330; DB 8; Pred. No. 2.1e-12;

Query Match Best Local Si RESULT 612

Query Match

Query Match

Query Match

Query Match Best Local S

RESULT 611

Score 330; DB 8; Length 653; Pred. No. 2.1e-12;

Length 653;

Score 330; DB 8; Pred. No. 2.1e-12;

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ADG07268 standard; protein; 653 AA.
Novel human secreted and transmembrane protein PRO1111.
US2003207350-A1.
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Novel human secreted and transmembrane protein PRO1111
US2003194778-A1.
                                                                                                                                                                                                                                                   Novel human secreted and transmembrane protein PRO1111.
US203207427-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              νουν/εζυ standard; protein; 653 AA.
Novel human secreted and transmembrane protein PRO1111.
US2002007356-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADG62083 standard; protein; 653 AA.
Novel human secreted and transmembrane protein PRO1111
US2003207428-A1.
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Novel human secreted and transmembrane protein PRO1111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADG60979 standard; protein; 653 AA.

Novel human secreted and transmembrane protein PRO1111
US2003207390-A1.
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GENOV-2003.
(GETH ) GENENTECH INC.
(GETY Match 10.5%; Score 330; DB 8;
Lery Match 24.3%; Pred. No. 2.1e-12;
Best Local Similarity 24.3%; Pred. No. 2.1e-12; RESULT 615
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                                                          ADG04070 standard; protein; 653 AA.
Human PRO polypeptide #219.
US2003207423-A1.
06-NOV-2003.
(GETH ) GENENTECH INC.
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Human PRO polypeptide #219.
US2003207358-A1.
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24.3%;
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Best Local Similarity 24.3%;
RESULT 622
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Best Local Similarity 24.3%;
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A (GETH) GENENTECH INC.

10 CBT 10 C
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity RESULT 618
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Best Local Similarity
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RESULT 617
                Score 330; DB 8; Length 653; Pred. No. 2.1e-12;
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Novel human secreted and transmembrane protein PRO1111.
US2003207389-A1.
06-NOV-2003.
(GETH ) GENENTECH INC.
10.5%; Score 330; DB 8; Length 653;
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Novel human secreted and transmembrane protein PRO1111
US2003207424-A1.
06-NOV-2003.
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CANDY-2003.

(GETH ) GENENTECH INC.

Ery Match 10.5%; Score 330; DB 8;

Ery Match 24.3%; Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
                                                                        Human PRO polypeptide #219.
US2003599-A1.
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Human PRO polypeptide #219.
US2003207425-A1.
                                                                                                                                                                                                                                                                                                   ADG05283 standard, protein; 653 AA.
Human PRO polypeptide #219.
US2003207375-A1.
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Human PRO polypeptide #219.
US2003219885-A1.
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Human PRO polypeptide #219.
US2003207371-A1.
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(GENOV-2003.
(GETH ) GENENTECH INC.
10.5%;
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06-NOV-2003.

(GETH ) GENENTECH INC.

Match 10.5%;
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06-NOV-2003.
(GETH ) GENENTECH INC.
Match '...itv 24.3%;
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24.3%;
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24.3%;
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24.3%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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             Query Match
Best Local Similarity
RESULT 606
ID ADG16824 standard; p:
DE Human PRO polypeptid
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH IN
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Best Local Similarity
RESULT 608
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Best Local Similarity
RESULT 607
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Score 330; DB 8; Length 653; Pred. No. 2.1e-12;

us-09-943-780-69.ragspdi

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Human PRO polypeptide #219.
US2003077723-A1.
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                ADG56971 standard; protein; 653 AA.
Novel human secreted and transmembrane protein PRO1111.
05.2003207364-A1.
06-WOV-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                          ADG55867 standard; protein; 653 AA.
Novel human secreted and transmembrane protein PRO1111.
US2003207365-A1.
06-NOV-2003.
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Novel human secreted and transmembrane protein PRO1111.
US2003207420-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADG58075 standard; protein; 653 AA.
Novel human secreted and transmembrane protein PRO1111.
US2003207363-A1.
06-NOV-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                   ADGS8627 standard; protein; 653 AA.
Novel human secreted and transmembrane protein PRO1111
US2003207368-A1.
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Novel human secreted and transmembrane protein PRO1111.
US2003207415-A1.
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Novel human secreted and transmembrane protein PRO1111
US2003207421-A1.
                                                                                                          Score 330; DB 8;
Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
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US2003228656-A1.
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RESULT 630
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Best Local Similarity 24.3%;
RESULT 633
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24TY Match
Best Local Similarity 2.
RESULT 629
ID ADG53659 stand?
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PN US20032.
PD 06.2
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(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-DEC-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                   (GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                             Best Local Similarity
RESULT 626
ID ADG58627 standard; pr
DE Novel human secreted
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GETH ) GENENTECH INC.
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                                                                                                                     Best Local Similarity
RESULT 625
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                                                                                                                                                                                                                                                   Query Match
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RESULT (
ID ADK
DE NO
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Length 653;
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                                                                                                                                                                                                                               Novel human secreted and transmembrane protein PRO1111. US2003207414-A1.
                                                                                                                                                                                                                                                                                                                                                                                     ADG54211 standard; protein; 653 AA.
Novel human secreted and transmembrane protein PRO1111.
US2003207416-A1.
                                                                                                 ADH12061 standard; protein; 653 AA.
Novel human secreted and transmembrane protein PRO1111
US2003207419-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADG61531 standard; protein; 653 AA.
Novel human secreted and transmembrane protein PRO1111.
US2003207429-A1.
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Novel human secreted and transmembrane protein PRO1111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADH12685 standard; protein; 653 AA.
Novel human secreted and transmembrane protein PRO1111
US2003207378-A1.
                                                   Score 330; DB 8;
Pred. No. 2.1e-12;
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(GETH) GENENTECH INC.
(ery Match 10.5%; Score 330; DB 8;
                                                                                                                                                                                            Score 330; DB 8;
Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
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Query Match
10.5%; Score 330; DB 8;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
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Pred. No. 2.1e-12
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Pred. No. 2.1e-12;
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Human secreted/transmembrane protein PRO1111.
US2003224358-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADH20008 standard; protein; 653 AA.
Human secreted/transmembrane protein PRO1111.
US2003219856-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADG81180 standard; protein; 653 AA.
Human PRO polypeptide #219.
US2003194793-A1.
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06-NOV-2003.
(GETH ) GENENTECH INC.
wetch 10.5%; S.
US20050.
24-APR-2003.
(GETH ) GENENTECH INC.
MATCh ... 12 10 5%;
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RESULT 642
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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                                             Query Match
Best Local Similarity
RESULT 634
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Best Local Similarity
RESULT 636
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RESULT 637
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Best Local Similarity
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3 5 3 5 5	ovel human secreted and transme \$2003207377-A1. \$2003207377-A1. \$2.NOV-2003. BENOV-2003. Match 10.5%; Scc Local Similarity 24.3%; Pre Local Similarity 24.3%; Pre D659803 standard; protein; 653 \$2003207369-A1. \$2003207369-A1.	VILT 646  VILT 646  VILT 646  VILT 647  VILT 6	PN US2004009548-A1. PD 15-JAN-2004. PA (GETH) GENENTECH INC.  OMETY MAtch Best Local Similarity 24.3%; Score 330; DB 8; Length 653;  RESULT 648  ID AD115441 standard; protein; 653 AA.  DE NOVP-1 human secreted and transmembrane protein PRO1111.  PD 06-NOV-2003.  PA (GETH) GENENTECH INC.  OMETY MATCH Best Local Similarity 24.3%; Pred. No. 2.1e-12;  Best Local Similarity 24.3%; Pred. No. 2.1e-12;	RESULT 649  ID ADG09318 standard; protein; 653 AA.  DE Novel human secreted and transmembrane protein PRO1111.  PN US2004009547-A1.  PN US2004009547-A1.  PD 15-2AA-2004.  PA (GETH) GENENTECH INC.  Query Match  Best Local Similarity 24.3%; Pred. No. 2.1e-12;  RESULT 650  ID AD114773 standard; protein; 653 AA.  DE Novel human secreted and transmembrane protein PRO1111.	US2003207383-A1.  GG-NOV-2003.  (GFTH) GENENTECH INC.  10.5%; Score 330;  Sest Local Similarity 24.3%; Pred. No.  SULT 651  AD118368 standard; protein; 653 AA.  Novel human secreted and transmembrane US2003207349-A1.  06-NOV-2003.

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ADS98753 standard; protein; 824 AA.
Protein factor discovery related human contig polypeptide, SEQ ID 1017.
WO2004087874-A2.
Best Local Similarity 24.6%; Pred. No. 2.5e-12; RESULT 668
                                                                  (NUVE-) NUVELO INC. (DRWA/) DRMANAC R T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AEB14155 standard; protein; 653 AA.
Cancer cell diagnosis method-related human protein - SEQ ID 438.
US2005153396-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABG98014 standard; protein; 649 AA.

Human leucine rich repeat domain protein associated protein #1.

WO200274959-A2.

O 26-SEP-2002.

A (BRIM) BRISTOL-MYERS SQUIBB CO.

Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 6; Length 775
    10.5%; Score 330; DB 8; Length 653; 24.3%; Pred. No. 2.1e-12;
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                                                                                                                Length 653;
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Pred. No. 2.1e-12;
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                                                                                                              Score 330; DB 8;
Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
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Pred. No. 2.1e-12;
                                                                                                                                                    ADZ03409 standard; protein; 653 AA.
Human secreted/transmembrane PRO1111 protein.
US2005074837-A1.
                                                                                                                                                                                                                                                                                                                                                                        AEA23332 standard; protein; 653 AA.
Tumor antigen of hematopoietic origin TAHO15.
W0200549075-A2.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                              AEA38492 standard; protein; 653 AA.
Human secreted/transmembrane protein, #132.
US2005112725-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABU12069 standard; protein; 775 AA.
Human NOV15a CG92531-01 protein SEQ ID
                                        AD703358 standard; protein; 653 AA.
Human PRO polypeptide #219.
US2004214269-A1.
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RESULT 664
                                                                                                             10.5%;
24.3%;
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Local Similarity 24.3%;
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(GETH ) GENENTECH INC.
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GODOWSKI P J.
GURNEY A L.
SHERWOOD S.
                                                                                                 (GETH ) GENENTECH INC.
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GERRITSEN M E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMITH V.
STEWART T A.
TUMAS D.
WATANABE C K.
                                                                                                                                                                                               07-APR-2005.
(GETH ) GENENTECH INC
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DEFORGE L.
DESNOYERS L.
FILVAROFF E.
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                                                                                                                                                                                                                                   Best Local Similarity RESULT 663
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            Best Local Similarity RESULT 661
                                                                                                             Query Match
Best Local Similarity
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17-OCT-2002.
                                                                                 28-OCT-2004
    Query Match
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RESULT 662
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ADA06943 standard; protein; 627 AA.

Human PRO polypeptide #50.
US2003068781-A1.
10-APR-2003.
(GETH ) GENENTECH INC.
ery Match
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         Length 824;
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Human secreted/transmembrane polypeptide PRO34192.
US2003068780-A1.
                                                                                                                                                                                                                                                                                                                                                       ADA43797 standard; protein; 627 AA.
Human secreted/transmembrane polypeptide PRO34192
US2003064474-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human secreted/transmembrane polypeptide PRO34192 US2003073196-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADA43681 standard; protein; 627 AA.
Human secreted/transmembrane polypeptide PRO34192
US2003073190-A1.
                                                                                                                                                     Score 328.5; DB 5;
Pred. No. 2.5e-12;
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Pred. No. 2.5e-12;
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Pred. No. 2.5e-12;
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Pred. No. 2.5e-12;
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       10.5%; Score 329; DB 8; 25.5%; Pred. No. 3.3e-12;
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Pred. No. 2.5e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human PRO polypeptide #50.
                                                         ABG34079 standard; protein; 627 AA.
Human Pro peptide #51.
WO200224888-A2.
                                                                                                                                                                                                        ADA01368 standard; protein; 627 AA. Human PRO polypeptide #50. US2003068779-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADA43565 standard; protein; 627 AA.
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PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 24.2%;
RESULT 672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.5%;
24.2%;
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PA (GETH ) GENENTECH INC.

QUELY MATCh 10.5%;

Best Local Similarity 24.2%;

RESULT 674
                                                                                                                                                   Query Match 10.5%;
Best Local Similarity 24.2%;
RESULT 670
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Best Local Similarity 24.2%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                                                28-MAR-2002.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 673
Query Match
Best Local Similarity
RESULT 669
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RESULT 686
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(GETH ) GENENTECH INC.
ery Match 10.5%; Score 328.5; DB 7; Length 627;
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(GETH ) GENENTECH INC.
(GETH ) GENENTECH INC.
ery Match
10.5%; Score 328.5; DB 7; Length 627;
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                                                                                                                              Score 328.5; DB 7; Length 627;
Pred. No. 2.5e-12;
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                                     ADA08431 standard; protein; 627 AA.
Novel human secreted and transmembrane protein PRO34192.
US2003068783-A1.
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Novel human secreted and transmembrane protein PRO34192.
US2003082731-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADB66046 standard; protein; 627 AA.
Human secreted/transmembrane polypeptide PRO34192
US2003082732-A1.
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US2003082729-A1.
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Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 684
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Pred. No. 2.5e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 328.5; DB 7;
Pred. No. 2.5e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D ADB99840 standard, protein; 627 AA.

Human PRO polypeptide SEQ ID 100.

N US2003073192-Al.

N US2003073192-Al.

N US2003073192-Al.

A (GETH) GENENTECH INC.

Query Match

10.5%; Score 328.5; DB 7

Best Local Similarity 24.2%; Pred. No. 2.5e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.5%; Score 328.5; DB 7, 24.2%; Pred. No. 2.5e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADC23444 standard; protein; 627 AA.
Human transmembrane PRO polypeptide (SeqID 100)
US2003073193-A1.
     24.2%; Pred. No. 2.5e-12;
                                                                                                                                                                        Human PRO polypeptide SEQ ID 100.
USZO03082728-A1.
                                                                                                                                                                                                                                                                                                                       JADB87007 standard; protein; 627 AA.
Human PRO polypeptide #50.
US2003082726-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein; 627 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADC26137 standard; protein; 627 AA.
Human PRO34192 protein.
US2003073194-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US2003cc.
01-MX-2003.
(GETH ) GENENTECH INC.
"arch "raity 24.2%;
                                                                                                                              10.5%;
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24.2%;
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                                                                                        10-APR-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
RESULT 682
ID ADB99495 standard; pr
DE Novel human secreted
PN US2003082731-A1.
PD 01-NAY-2003.
PA (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
RESULT 680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity RESULT 685
Best Local Similarity RESULT 677
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Best Local Similarity
RESULT 683
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Best Local Similarity
                                                                                                                                           Best Local Similarity RESULT 678
                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
RESULT 679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best_Local Similarity RESULT 681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADB66162 standard;
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Score 328.5; DB 7; Length 627; Pred. No. 2.5e-12;
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A (GETH) GENENTECH INC.
Ouery Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.5%; Score 328.5; DB 7; Length 627; 24.2%; Pred. No. 2.5e-12;
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Pred. No. 2.5e-12;
                                                                                     Score 328.5; DB 7; Length 627; Pred. No. 2.5e-12;
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US2003078401-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                  ADD95496 standard; protein; 627 AA.
Human secreted/transmembrane polypeptide PRO34192.
US2003064473-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human secreted/transmembrane polypeptide PRO34192
US2003073188-A1.
                                                                                                                                                                                                                                                                                                                                                                Score 328.5; DB 7;
Pred. No. 2.5e-12;
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17-APR-2003.
(GETH ) GENENTECH INC.
10.5%; Score 328.5; DB 7;
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Pred. No. 2.5e-12;
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Pred. No. 2.5e-12;
                                                                                                                                     ADE11270 standard; protein; 627 AA. Human PRO polypeptide #50. USZ003073191-A1. USZ003073191-A1. (GETH.) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lucare standard; protein; 627 AA. Human PRO polypeptide #50. US2003073195-A1.
ADE04964 standard, protein, 627 AA.
Human PRO polypeptide #50.
US2003068778-A1.
10-APR-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADD88317 standard; protein; 627 AA.
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                                                                                                                                                                                                                                                                                protein; 627 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADE38201 standard; protein; 627 AA
                                                                                                                                                                                                                                                                                                              US200305...
01-MAY-2003.
(GETH) GENENTECH INC.
10.5%;
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                                                                                     Watch 10.5%; Local Similarity 24.2%;
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Best Local Similarity 24.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human PRO polypeptide #50.
US2003119120-A1.
26-JUN-2003.
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US2003073189-A1.
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US2003082733-A1.
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(GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
RESULT 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity RESULT 695
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ID ADF99453 standard;
                                                                                                                                                                                                                                                                                ADD88201 standard;
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RESULT 687
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Score 328.5; DB 7; Length 627; Pred. No. 2.5e-12;
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                                                                                                                                                                                                                                                                                                                                                                                 DB 7; Length 627;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vuery Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 10.5%; Score 328.5; DB 8; Length 627; Best Local Similarity 24.2%; Pred. No. 2.5e-12; RESULT 704
                                                                                                                                                                                                                                      DB 7; Length 627;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 328.5; DB 8; Length 627;
Pred. No. 2.5e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.5%; Score 328.5; DB 8; Length 627; 24.2%; Pred. No. 2.5e-12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADE51867 standard; protein; 627 AA.
Human secreted/transmembrane polypeptide PRO34192.
US2003104561-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADE37609 standard; protein; 627 AA.
Human secreted/transmembrane polypeptide PRO34192.
022003104565-A1.
05-JUN-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                 ADE51751 standard; protein; 627 AA,
Human secreted/transmembrane polypeptide PRO34192
US2003104560-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADE37725 standard; protein; 627 AA.
Human secreted/transmembrane polypeptide PRO34192
US2003104564-A1.
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US2003138901-A1.
                                                                                                                                                                                                                                      Score 328.5; DB 7
Pred. No. 2.5e-12;
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ADG06546 standard; protein; 627 AA.
Human PRO polypeptide #50.
US2003077742-A1.
                                                                                                                                                                                                                                                                                      ADG82498 standard; protein; 627 AA.
Human PRO polypeptide #50.
US2003077744-Al.
24-APR-2003.
                                                                                                                                               protein; 627 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADE38080 standard; protein; 627 AA.
Human PRO polypeptide #50.
US2003104566-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADE76169 standard; protein; 627 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  627 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.5%;
24.2%;
                                            PD 24-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 10.5%;

Best Local Similarity 24.2%;
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24.2%;
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RESULT 703
                                                                                                                                                                                                                                                                                                                                                                                                  24.2%;
                                                                                                                                         ADG05497 standard, protein,
Human PRO polypeptide #50.
US2003077741-A1.
24-ARR-2003.
(GETH ) GENENTECH INC.
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A ) GENENTECH I.

FY Match

Best Local Similarity .

RESULT 697

ID ADG82498 standa-

DE Human PRO r

PD 24-
PA 24-
PA
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(GETH ) GENENTECH INC.
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2003.

AT 9 GENENTECH 1.

AT 9 MATCh
BEST LOCAL SIMILATITY 2.

RESULT 698
ID ADES1751 stand?
DE Human secre
PN US20031.
PD 05-
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                             (GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity RESULT 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity RESULT 699
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Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 705
ID ADE39492 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003119117-A1.
PD 26-JUN-2001
                                                                                                                                                                                                                            Score 328.5; DB 8; Length 627; Pred. No. 2.5e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 328.5; DB 8; Length 627; Pred. No. 2.5e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 328.5; DB 8; Length 627; Pred. No. 2.5e-12;
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Pred. No. 2.5e-12;
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Human secreted/transmembrane polypeptide PRO34192
US2003124666-A1.
                                                                                                                                                                                                                                                                                                                                                           Score 328.5; DB 8;
Pred. No. 2.5e-12;
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Pred. No. 2.5e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 328.5; DB 8
Pred. No. 2.5e-12;
                                                                                                                                                                                                                                                                          ADE04296 standard; protein; 627 AA.
Human PRO polypeptide #50.
US2003096364-A1.
                                                                                                                                                                                                                                                                                                                                                                                                       ADE39893 standard; protein; 627 AA. Human PRO polypeptide #50. US2003138896-A1. C4-JUL-2003. (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADE65444 standard; protein; 627 AA.
Human PRO polypeptide #50.
US2003119116-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADE76053 standard; protein; 627 AA.
Human PRO polypeptide #50.
US2003124663-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADE64574 standard; protein; 627 AA.
Human PRO polypeptide #50.
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22-MAY-2003.
(GETH ) GENENTECH INC.
Watch 10.5%; Sr
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PA (GETH ) GENENTECH INC.
Query Match 10.5%;
Best Local Similarity 24.2%;
RESULT 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 24.2%;
RESULT 708
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RESULT 712
                                                                                                                                                                                          PD 26-JUN-2003.

PA (GETH ) GENENTECH INC.

QUETY MATCh 10.5%;

BEST LOCAL Similarity 24.2%;

RESULT 706
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Best Local Similarity 24.2%;
RESULT 711
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
RESULT 707
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RESULT 709
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Score 328.5; DB 8; Length 627; Pred. No. 2.5e-12;
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Pred. No. 2.5e-12;
                                                        Score 328.5; DB 8; Length 627; Pred. No. 2.5e-12;
                                                                                                                                                                                         DB 8; Length 627;
                                                                                                                                                                                                                                                                                                                          Length 627;
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                                                                                                                                                                                                                                      ADE51983 standard; protein; 627 AA.
Human secreted/transmembrane polypeptide PRO34192
US2003104562-A1.
                                                                                                                                                                                                                                                                                                                                                                     ADD91014 standard; protein; 627 AA.
Human secreted/transmembrane polypeptide PRO34192
US2003138902-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human secreted/transmembrane polypeptide PRO34192 US2003104563-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADD90169 standard; protein; 627 AA.
Human secreted/transmembrane polypeptide PRO34192
US2003138904-A1.
                                                                                                                                                                                                                                                                                                                         Score 328.5; DB 8;
Pred. No. 2.5e-12;
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Pred. No. 2.5e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 328.5; DB 8;
Pred. No. 2.5e-12;
                                                                                                                     Human PRO polypeptide #50.
US2003096363-A1.
22-MAY-2003.
(GETH) GENENTECH INC.
10.5%; Score 328.5; DB 8; Local Similarity 24.2%; Pred. No. 2.5e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 328.5; DB 8 Pred. No. 2.5e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADE38793 standard; protein; 627 AA. Human PRO polypeptide #50. US2003108996-A1. 12-JUN-2003. (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADE39608 standard; protein; 627 AA.
Human PRO polypeptide #50.
US2003119118-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADE38677 standard; protein; 627 AA.
Human PRO polypeptide #50.
US2003119086-A1.
                                                                                                       protein; 627 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADE06309 standard; protein; 627 AA.
Human PRO polypeptide #50.
US2003138898-A1.
                                                                                                                                                                                                                                                                       US2003....
05-JUN-2003.
(GETH) GENENTECH INC.
"orch 'Town 10.5%; Sc
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24-JUL-2003.
(GETH ) GENENTECH INC.
10.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USZUCZ-203.
24-JUL-2003.
(GETH ) GENENTECH INC.
Match 'larity 24.2%;
                                                       10.5%;
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PA (GETH ) GENENTECH INC.

QUETY MATCh

BEST LOCAL Similarity 24.2%;

RESULT 717
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24.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUN-2003.
(GETH ) GENENTECH INC.
                      26-JUN-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GETH ) GENENTECH INC.
L4-A1.

2003.

LH ) GENENTECH LCT MATCH LOCAL SIMILARITY THE ID ADB38909 stands PN US20030.

PN US20030.

PD 22-V.
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Best Local Similarity
RESULT 720
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Best Local Similarity
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Best Local Si
RESULT 716
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RESULT 719
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Score 328.5; DB 8; Length 627;
Pred. No. 2.5e-12;
                                     8; Length 627;
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Pred. No. 2.5e-12;
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Pred. No. 2.5e-12;
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Pred. No. 2.5e-12;
                                                                                                                                                                        DB 8; Length 627;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Angl1998 standard; protein; 627 AA.
Human secreted/transmembrane polypeptide PRO34192.
US2003077743-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADE77452 standard; protein; 627 AA.
Human secreted/transmembrane polypeptide PRO34192
US2003124667-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADE38561 standard; protein; 627 AA.
Human secreted/transmembrane polypeptide PRO34192
US2003104559-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADG11114 standard; protein; 627 AA.
Human secreted/transmembrane polypeptide PRO34192
US2003170809-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 8;
                                 Score 328.5; DB 8 Pred. No. 2.5e-12;
                                                                                                                                                                      Score 328.5; DB 8;
Pred. No. 2.5e-12;
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                                                                                                                                                                                                                                                                                                           Score 328.5; DB 8 Pred. No. 2.5e-12;
                                                                                   ADD89213 standard; protein; 627 AA.
Human PRO polypeptide #50.
US2003138897-A1.
                                                                                                                                                                                                                      ADD89980 standard; protein; 627 AA.
Human PRO polypeptide #50.
US2003138899-A1.
24-UUL-2003.
                                                                                                                                                                                                                                                                                                                                                             protein; 627 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADE65328 standard; protein; 627 AA. Human PRO polypeptide #50. US2003119113-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein; 627 AA
                                                                                                                   10.5%;
24.2%;
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24.2%;
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RESULT 728
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24.2%;
PD 26-JUN-2003.

PA (GETH) GENENTECH INC.

QUETY MATCh 10.5%;

Best Local Similarity 24.2%;

RESULT 723
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Best Local Similarity 24.2%;
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US2003119115-A1.
26-JUN-2003.
(GETH ) GENENTECH INC.
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US2003138900-A1.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                 (GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity RESULT 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
RESULT 730
                                                                                                                                                                                   Best Local Similarity RESULT 724
                                                                                                                                                                                                                                                                                                                      Best Local Similarity RESULT 725
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
RESULT 726
                                                                                                                                                                                                                                                                                                                                                           ADE19874 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADE39376 standard;
                                                                                                                                                                                                                                                                                                                                                                                                             24-JUL-2003
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Length 627;

Length 627;

Length 627;

8

RESULT 734

A D E E E

Length 627;

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Length 627;

DB 8;

Length 627;

DB 8;

Length 627;

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Length 627;

Length 627;

DB 8;

Best Loca RESULT 740

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ADH52423 standard; protein; 627 AA.
Novel human secreted and transmembrane protein PRO34192.
US2003119130-A1.
26-JUN-2003.
(GETH ) GENENTECH INC.
ery Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADH49503 standard; protein; 627 AA.
Novel human secreted and transmembrane protein PRO34192.
US2003119127-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADH51967 standard; protein; 627 AA.
Novel human secreted and transmembrane protein PRO34192.
US2003119125-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADH49822 standard; protein; 627 AA. Novel human secreted and transmembrane protein PRO34192. US2003119128-A1.
   Score 328.5; DB 8;
Pred. No. 2.5e-12;
                                                         ADH23828 standard; protein; 627 AA.
Human secreted/transmembrane polypeptide PRO34192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADH29288 standard; protein; 627 AA.
Human secreted/transmembrane polypeptide PRO34192
                                                                                                                                               Score 328.5; DB 8;
Pred. No. 2.5e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-JUN-2003.
(GETH ) GENENTECH INC.
Query March
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 328.5; DB 8
Pred. No. 2.5e-12;
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Pred. No. 2.5e-12;
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Pred. No. 2.5e-12;
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Pred. No. 2.5e-12;
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Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 749
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Pred. No. 2.5e-12;
                                                                                                                                                                                                 ADH40203 standard; protein; 627 AA.
Human PRO34192 protein.
US2003119132-A1.
                                                                                                                                                                                                                                                                                                                                   ADH40088 standard; protein; 627 AA.
Human PRO34192 protein.
US2003119133-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         627 AA
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-2003.
) GENENTECH INC.
10.5%; ?
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   10.5%;
24.2%;
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24.2%;
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24.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADH31410 standard; protein;
Human PRO polypeptide #50.
US2003119138-A1.
26-JUN-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
QUETY MATCh 10.5%;
Best Local Similarity 24.2%;
RESULT 747
                                                                                     USZU03119142-A1.
26-JUN-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                              26-JUN-2003
(GETH ) GENENTECH INC.
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26-JUN-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
RESULT 743
                  Best Local Similarity
RESULT 741
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RESULT 745
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RESULT 744
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RESULT 746
                                                                                                                                                             Best Local Similarity
RESULT 742
                                                     ADH23828 standard;
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                                                                                                                                             Query Match
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     Query Match
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                  Score 328.5; DB 8; Length 627; Pred. No. 2.5e-12;
                                                                                                                                                            Length 627;
                                                                                                                                                                                                                                                                                                   Score 328.5; DB 8; Length 627; Pred. No. 2.5e-12;
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Novel human secreted and transmembrane protein PRO34192.

V US2003119124-A1.

S G-JUN-2003.

A (GFTH ) GENEWIECH INC.

10.5%; Score 328.5; DB 8; Length
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Novel human secreted and transmembrane protein PRO34192
US2003119123-A1.
                                                                                                                                                                                                                              Human secreted/transmembrane polypeptide PRO34192
US2003103140-A1.
26-UTW-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                          10.5%; Score 328.5; DB 8; 24.2%; Pred. No. 2.5e-12;
                                                                                                                                                                                                                                                                                                                                                                        Human secreted/transmembrane polypeptide PRO34192
US2003119137-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADH23712 standard; protein; 627 AA.
Human secreted/transmembrane polypeptide PRO34192
US2003119143-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADH27042 standard; protein; 627 AA.
Human secreted/transmembrane polypeptide PRO34192
US2003119135-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADH26926 standard; protein; 627 AA.
Human secreted/transmembrane polypeptide PRO34192.
US2003119134-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADH18890 standard; protein; 627 AA.
Human secreted/transmembrane polypeptide PRO34192.
US2003119141-A1.
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Pred. No. 2.5e-12;
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Pred. No. 2.5e-12;
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                                                                  ADH31526 standard; protein; 627 AA.
Human PRO polypeptide #50.
US2003119139-A1.
                                                                                                                                                                                                                                                                                                                                                           627 AA.
                                                                                                                                                                                                                 627 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US200JILL.
26-JUN-2003.
(GETH ) GENENTECH INC.
March 10.5%; S'
                                                                                                                                                                                                                                                                                                   10.5%;
              10.5%;
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24.2%;
                                                                                                                                                                                                            ADH38774 standard; protein;
                                                                                                                                                                                                                                                                                                                                                       ADH29409 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-JUN-2003.
(GETH ) GENENTECH INC.
                                                                                                                      26-JUN-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                             26-JUN-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-JUN-2003.
(GETH ) GENENTECH INC.
(GETH ) GENENTECH INC
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(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-JUN-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                         Best Local Similarity RESULT 733
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
RESULT 735
                Query Match
Best Local Similarity
RESULT 732
                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity RESULT 739
                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
```

RESULT 736

A S S E E

BESE

RESULT 737

A D M E E

Length 810;

Length 628

Length 811;

```
AAG55805 standard; protein; 628 AA.
Human leucine-rich repeat (LRR) family member, 33395 polypeptide.
WO200172827-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Amino acid sequence of an interferon omega-1 like protein NOV2. WO200142471-A2. 14-JUN-2001. (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.3%; Score 322.5; DB 6; Length 811; 22.0%; Pred. No. 8.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 10.3%; Score 322.5; DB 8; Length 811;
Best Local Similarity 22.0%; Pred. No. 8.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADQ21196 standard; protein; 811 AA.
Human soft tissue sarcoma-upregulated protein - SEQ ID 4016.
WQ2004048938-AZ.
10-JUN-2004.
(PROT-) PROTEIN DESIGN LABS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAG67523 standard; protein; 628 AA.
Amino acid sequence of a human secreted polypeptide.
WO200166690-A2.
                                                                                                                                                                                                                                                                                                                                                                               PD 27-MAR.2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match
10.3%; Score 322.5; DB 6;
Best Local Similarity 22.0%; Pred. No. 8.3e-12;
RESULT 762
                                                                                                                                                                                                                                                                                    Score 322.5; DB 7;
Pred. No. 8.2e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 322.5; DB 7;
Pred. No. 8.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAO23114 standard, protein, 811 AA.
KIAA0644 'human modifier of p53 pathway' protein
                                                                                                        Best Local Similarity 24.1%; Pred. No. 4.9e-12; RESULT 760
                                                                                                                                                                       ADN95165 standard; protein; 810 AA.
Human BEC/LEC-related protein sequence SeqID87.
WO2003080640-A1.
02-OCT-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.3%; Score 322; DB 8; 36.2%; Pred. No. 6.3e-12;
                                                                                                                                                                                                                                                                                                                                    ABR58642 standard; protein; 811 AA.
Human cancer related protein SEQ ID NO:299
WO2003025138-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADN95110 standard; protein; 811 AA. Human LEC protein sequence SeqID32. WO2003080640-A1. 02-OCT-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADR45590 standard; protein; 605 AA Homologue of IRSG-1, baboon ALS. US2004176296-A1.
(MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (LUDW-) LUDWIG INST CANCER RES. (LICN ) LICENTIA LTD.
                                                                                                                                                                                                                                                 (LUDW-) LUDWIG INST CANCER RES. (LICN ) LICENTIA LTD.
                                                                  WOLCOTTONION PHARM INC. (MILL-) MILLENNIUM PHARM INC. 10.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.3%;
                                                                                                                                                                                                                                                                                     10.3%;
22.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2003.
(EXEL-) EXELIXIS INC.
                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
RESULT 761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity RESULT 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity RESULT 764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2003035833-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                  Score 328.5; DB 8; Length 627; Pred. No. 2.5e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 627;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.5%; Score 328.5; DB 8; Length 627; 24.2%; Pred. No. 2.5e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 627;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-SEP-2004.
(SAGR-) SAGRES DISCOVERY INC.
ery Match 10.3%; Score 324; DB 8; Length 626;
                                                                                                                                                                           Novel human secreted and transmembrane protein PRO34192. US200119121-A1.
                                                                                                                                                                                                                                                                                                                                    AH/151851 standard; protein; 627 AA.
Novel human secreted and transmembrane protein PRO34192.
US2003119126-A1.
26-JUN-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADIJ3609 standard; protein; 627 AA.
Novel human secreted and transmembrane protein PRO34192.
US2003119131-A1.
26-JUN-2003.
(GETH ) GENENTECH INC.
                                    ADH52539 standard; protein; 627 AA. Novel human secreted and transmembrane protein PRO34192. US2003119129-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADH58412 standard; protein; 627 AA.
Novel human secreted and transmembrane protein PRO34192.
US2003119122-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                   10.5%; Score 328.5; DB 8; 24.2%; Pred. No. 2.5e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OSZUN-2003.
(GETH) GENENTECH INC.
(GETH) GENENTECH INC.
(ery Match 10.5%; Score 328.5; DB 8;
ery Match 24.2%; Pred. No. 2.5e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADLOBGOG standard; protein; 627 AA.
Human secreted/transmembrane polypeptide PRO34192
US2003186372-A1.
                                                                                                                                                                                                                                                                                    Score 328.5; DB 8;
Pred. No. 2.5e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 327.5; DB 4;
Pred. No. 3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 328.5; DB 8;
Pred. No. 2.5e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 328.5; DB 8 Pred. No. 2.5e-12;
   24.2%; Pred. No. 2.5e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse cancer-associated protein; 626 AA.
Mouse cancer-associated protein MP14-035.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human secreted protein, 636 AA.
Novel human secreted protein #3361.
25-OCT-2001.
(HYSE) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADK00865 standard, protein, 627 AA.
Human PRO polypeptide #50.
US2003186373-A1.
                                                                                                                                  10.5%;
24.2%;
                                                                                                                                                                                                                             US2003...
26-UN-2003.
(GETH ) GENENTECH INC.
"arch "reity 24.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.5%;
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24.2%;
                                                                                           26-JUN-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-OCT-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-OCT-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
RESULT 753
ID ADH58412 standard; pl
DE Novel human secreted
PN US2003119122-A1.
PD 26-UUN-2003.
PA (GETH ) GENENTECH INC
                                                                                                                                           Best Local Similarity
RESULT 751
ID ADH58536 standard; pi
DE Novel human secreted
PN US2003119121-A1.
PD 26-UNA-2003.
PA (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Luery Match
Best Local Similarity
RESULT 758
ID ABO84499 --
Best Local Similarity
RESULT 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity RESULT 755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
RESULT 757
                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
RESULT 752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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Best Local Similarity
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Best Loca RESULT 754

RESULT 756

Length 605;

RESULT

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(RAMA/) RAMANATHAN C S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENENTECH INC.
BAKER K P.
FERRARA N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GODDARD A.
GODOWSKI P J.
GURNEY A L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-JAN-2002.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GERBER H.
GERRITSEN M E.
                                Best Local Similarity RESULT 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity RESULT 783
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GODO/)
(GURN/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (FERR/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (dopp/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABO04503 standard; protein; 628 AA.
Human cancer-associated protein HP14-035.4.
WOZO04074220-A2.
02-SEP-2004.
(SAGR-) SAGRES DISCOVERY INC.
10.2%; Score 321; DB 8; Length 628; set Local Similarity 23.9%; Pred. No. 7.6e-12;
   10.2%; Score 321; DB 4; Length 628; 23.9%; Pred. No. 7.6e-12;
                                                                                                                                                                                                                                                                              Length 628;
                                                                                                                                                                                                                                                                                                                                                                                                        vuery Match
10.2%; Score 321; DB 8; Length 628;
Best Local Similarity 23.9%; Pred. No. 7.6e-12;
RESULT 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 10.2%; Score 321; DB 8; Length 628; Best Local Similarity 23.9%; Pred. No. 7.6e-12; RESULT 772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PD 02-SEP-2004.

PA (SAGR-) SAGRES DISCOVERY INC.

Query Match 10.2%; Score 321; DB 8; Length 628;

Best Local Similarity 23.9%; Pred. No. 7.6e-12;

RESULT 773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.2%; Score 321; DB 6; Length 762; 25.5%; Pred. No. 9.6e-12;
                                                                                                                                           Length 628;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.2%; Score 321; DB 8; Length 628; 23.9%; Pred. No. 7.6e-12;
                                                                                                                                                                                            Luery Match
Best Local Similarity 23.9%; Score 321; DB 7; Len RESULT 770
ID ADH71652 standard; protein; 628 AA.
BN WO2003102155-A2.
PD 11-DEC-2003
                                                                                                                                                                                                                                                                                                                           ADH71652 standard; protein; 628 AA.
Human protein of the invention NOV22a SEQ ID NO:548.
WO2003102155-A2.
11-DEC-2003.
(CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADH71654 standard; protein; 628 AA.
Human protein of the invention NOV22b SEQ ID NO:550.
MO2003102155-A2.
(CURA-) CURAGEN CORP.
                                                                                                                                         Score 321; DB 5;
Pred. No. 7.6e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABO84501 standard; protein; 628 AA.

E Human cancer-associated protein HP14-035.2.

N W02004074320-A2.

D 02-SEP-2004.

10.2%; Score 321; DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABO84502 standard; protein; 628 AA.
Human cancer-associated protein HP14-035.3.
WO2004074320-A2.
                                                                                                                                                                                    ADF69107 standard; protein; 628 AA.
Human MP53 protein sequence SEQ ID NO:77.
WO2003083047-A2.
                                              ABP69326 standard; protein; 628 AA.
Human polypeptide SEQ ID NO 1373.
WO200270539-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABP70928 standard; protein; 762 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADI36917 standard; protein; 797 AA
                                                                                                                                        10.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ELIL ) LILLY & CO ELI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human LRR protein #12.
US2003220263-A1.
                                                                                                                                    Query Match
Best Local Similarity
RESULT 769
ID ADP69107 standard; pro
DE Human MP53 protein See
PN W02003083047-A2.
PD 99-OCT-2003.
PA (EXEL-) EXELIXIS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity RESULT 775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human LP341 protein.
WO2003029778-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
RESULT 774
Ouery Match
Best Local Similarity
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                                                                                                    12-SEP-2002.
(HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-NOV-2003.
(FEDE/) FEDER J N.
(MINT/) MINTIER G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Si
RESULT 776
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A S S S S S S

PORED

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ADS98018 standard; protein; 803 AA.
Protein factor discovery related isolated human polypeptide, SEQ ID 282.
WO2004081874-A2.
14-0CT-2004.
(NUVE-) NUVELO INC.
(DRMAA) DRMANAC R T.
                                                                                                                                                                                                                                                                                                                                                     PD 25-WAR-1999.

PA (GETH ) GENENTECH INC.

Querry Match

10.2%; Score 320; DB 2; Length 660;

Best Local Similarity 22.4%; Pred. No. 9.3e-12;

RESULT 779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DE AD078348 standard; protein; 660 AA.

DE Human PRO265 protein.

PN W0200015796-A2.

PD 23-MAR-2000.

PA (GETH) GENEWTECH INC.

Query Match 10.2%; Score 320; DB 3; Length 660;

Best Local Similarity 22.4%; Pred. No. 9.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ID AAB31208 standard; protein; 660 AA.

DB Amino acid sequence of human polypeptide PRO265.

PN WO200077037-A2.

PD 21-DEC-2000.

PA (GETH) GENENTECH INC.

Query Match 10.2%; Score 320; DB 4; Length 660;

Best Local Similarity 22.4%; Pred. No. 9.3e-12;
                                                                                                                                                                                                Query Match 10.2%; Score 321; DB 8; Length 803; Best Local Similarity 25.5%; Pred. No. 1e-11; RESULT 778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 660;
10.2%; Score 321; DB 8; Length 797; 25.5%; Pred. No. 1e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46.
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Human angiogenesis related protein PRO265 SBQ ID NO:
WO200208284-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adul2346 standard; protein; 660 AA.

Human PRO265 polypeptide sequence.
W0200140466-A2.
07-JUN-2001.
(GETH) GENENTECH INC.
ery Match
st Local Similarity 22.4%; Pred. No. 9.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PD 18-JAN-2001.

PA (GETH ) GENENTECH INC.

Query Match 10.2%; Score 320; DB 4;

Best Local Similarity 22.4%; Pred. No. 9.3e-12;

RESULT 781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 10.2%; Score 320; DB 5; Best Local Similarity 22.4%; Pred. No. 9.3e-12; RESULT 784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB84839 standard; protein; 660 AA.
Human PRO265 protein sequence SEQ ID NO:46.
WO200200690-A2.
                                                                                                                                                                                                                                                                              Amino acid sequence of protein, 660 AA.
W09914128-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB80217 standard; protein; 660 AA.
Human PRO265 protein.
WO200104311-A1.
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Query Match
Best Local Similarity
                                                                                                                      Query Match
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(GETH ) GENENTECH INC.
..... 10.2%; Score 320; DB 6; Length 660;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AB025179 standard; protein; 660 AA.
Novel human secreted and transmembrane protein PRO265.
US2003040014-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel human secreted and transmembrane protein PRO265.
US202197671-Al.
                                                                                                                                                                                                                                                                                                               ABO17790 standard; protein; 660 AA.
Novel human secreted and transmembrane protein PRO265
                                                                                                                                    Score 320; DB 5;
Pred. No. 9.3e-12;
                                                                                                                                                                                                                                                                 10.2%; Score 320; DB 6; 22.4%; Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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Human secreted/transmembrane protein PRO265.
US2003003530-A1.
02-JAN-2003.
(GETH ) GENENTECH INC.
10.2%; Score 320; DB
stry Match
tocal Similarity 22.4%; Pred. No. 9.3e-
                                                                                                                                                                              ABU71595 standard; protein; 660 AA.
Human PRO polypeptide #6.
US2002146709-A1.
IO-OCT-2002.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABU81044 standard; protein; 660 AA.
Human PRO polypeptide #175.
US2003004311-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABU66744 standard; protein; 660 AA.
Human PRO polypeptide #175.
US2003036180-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein; 660 AA
                                                                                                                                                                                                                                                                                                                      Abc..
Novel human bc..
US2003032156-A1.
13-FEB-2003.
(GETH ) GENENTECH INC.
**arch 10.2%; Sc
                                                                                                                                  10.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human PRO polypeptide #6.
US2002192659-A1.
19-DEC-2002.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-DEC-2002.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-FEB-2003.
(GETH ) GENENTECH INC.
                                                                 STEPHAN J F.
WATANABE C K.
WILLIAMS P M.
WOOD W I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-JAN-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                         Best Local Similarity
RESULT 786
ID ABO17790 standard; pr
DE Novel human secreted
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC
 HILLAN K J.
MARSTERS S A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
RESULT 788
ID AB025179 standard; pr
DE Novel human secreted
PN US2003040014-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC
                                                PAONI N F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity RESULT 790
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Best Local Similarity
RESULT 792
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RESULT 787
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Best Local Similarity
RESULT 791
                                                                                                                                                 Local Similarity
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Best Local Si
RESULT 785
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Best Local Si
RESULT 789
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(HILL/) H (MARS/) N (PANJ/) H (PAON/) H (STEP/) S (WATA/) W (WILL/) W (WOOD/) W
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Score 320; DB 6; Length 660;
Pred. No. 9.3e-12;
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                                                                                                                                                                            ncuo/29/ standard; protein; 660 AA.
Novel human secreted and transmembrane protein PRO265.
US203032063-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABU72065 standard; protein; 660 AA.
Novel human secreted and transmembrane protein PRO265.
US200217165-A1.
GB-NOV-2002.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUS9825 standard; protein; 660 AA.
Novel secreted and transmembrane protein PRO265.
US2003017563-A1.
23-JAN-2003.
(GEH) GENENTECH INC.
10.2%; Score 320; DB 6;
ery Match
st Local Similarity 22.4%; Pred. No. 9.3e-12;
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WCZCZ-2003.
(EXEL-) EXELIXIS INC.
(EXEL-) EXELIXIS INC.
ery Match
10.2%; Score 320; DB 6;
ery Match
22.4%; Pred. No. 9.3e-12;
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Human secreted/transmembrane polypeptide PRO265.
US2003044839-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABO25015 standard; protein; 660 AA.
Human secreted/transmembrane protein (PRO) #175.
US2003036179-A1.
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Pred. No. 9.3e-12;
   22.4%; Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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Pred. No. 9.3e-12,
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Pred. No. 9.3e-12
                                                                                                                                                                                                                                                                                                                                              AAO23116 standard; protein; 660 AA.
FLRT2 'human modifier of p53 pathway' protein.
WO2003035833-A2.
                                   ABU54352 standard; protein; 660 AA.
Human secreted/transmembrane protein PRO265.
US2002132240-A1.
19-SEP-2002.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABU64504 standard, protein, 660 AA.
Human secreted/transmembrane protein, #7.
US2002160374-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US200507...
06-MAR-2003.
(GETH ) GENENTECH INC.
407FCh 10.2%; St
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US2003023054-A1.
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20-FEB-2003.
(GETH ) GENENTECH INC.
...+ch ...-chv 22.4%;
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PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 22.4%;
RESULT 795
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22.4%;
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FESULT 800
                                                                                                                                      . Match
Local Similarity 22.4%;
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(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-OCT-2002.
(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 797
Best Local Similarity RESULT 793
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10.2%; Score 320; DB 6; Length 660; 22.4%; Pred. No. 9.3e-12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 660;
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Local Similarity 22.4%; Pred. No. 9.3e-12;
                                                                                                 Length 660;
                                                                                                                                                                                                                                                                                                                                                               Length 660;
           ABUG7166 standard; protein; 660 AA.
Novel human secreted and transmembrane protein PRO265.
US2003032062-A1.
13.FEB-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                          ABUG7020 standard; protein; 660 AA.
Human secreted/transmembrane, PRO, protein SEQ ID 350.
US2003032155-A1.
13.FEB-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                             ABU69627 standard; protein; 660 AA.
Novel human secreted and transmembrane protein PRO265.
US2003017463-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADA45869 standard; protein; 660 AA.
Novel human secreted and transmembrane protein PRO265.
US2003022328-A1.
30-JAN-2003.
(GETH ) GENENTECH INC.
                                                                                                                                           ABO14870 standard; protein; 660 AA.
Human secreted / transmembrane polypeptide PRO265.
US2003036060-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABO14809 standard; protein; 660 AA.
Human secreted / transmembrane polypeptide PRO265.
US2003027143-A1.
                                                                                                                                                                                                                                                                                                                                                             10.2%; Score 320; DB 6; 22.4%; Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
                                                                                             10.2%; Score 320; DB 6; 22.4%; Pred. No. 9.3e-12;
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Human secreted/transmembrane protein PRO265.
US2003032057-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADB29233 standard; protein; 660 AA.
Human secreted/transmembrane protein, #7.
US2003092002-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADA76300 standard; protein; 660 AA.
Human PRO polypeptide #175.
US2003073212-A1.
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22.4%;
                      CETH ) GENERAL OLD SECT (CETH ) GENERAL OLD SENDER IN SECULT 803 ID ABO14870 Standar DE Human Secretion US20030°

PN US20030°
PA
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
Query Match 1
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(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                         Best Local Similarity RESULT 804
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Best Local Similarity
RESULT 807
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RESULT 802
ID ABU671
DE Novel
PN US2003
PD 13-FEB
PA (GETH
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RESULT 809
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RESULT 810
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PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 820
                                                                                                                                                                                                                                                                                                                                                        PD 10-ARR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 814
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Pred. No. 9.3e-12;
                                                                                              Score 320; DB 6; Length 660;
Pred. No. 9.3e-12;
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Novel human secreted and transmembrane protein PRO265.

OLYMAY-20030

A (GETH) GENENTECH INC.

Ouery Match

Ouery Match
                                                                                                                                                                                                                                                                                                             ADB19358 standard; protein; 660 AA.
Novel human secreted and transmembrane protein PRO265.
US2003068796-A1.
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Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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Pred. No. 9:3e-12
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DE Human PRO polypeptide #175.

PN US2003073215-A1.

PD 17-APR-2003.

PA (GETH) GENENTECH INC.

QUETY MATCH

10.24; Score 320; DB

BESULT 818

ID ADA18089 standard; protein; 660 AA.

DE Human secreted/transmembrane protein, #7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABO32761 standard; protein; 660 AA.
Human secreted/transmembrane protein PRO265.
US2003045693-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human PRO polypeptide #175.
01-May ...
ADA18950 standard, protein, 660 AA.
Human PRO polypeptide #175.
US2003054517-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADB15942 standard; protein; 660 AA.
Human PRO polypeptide #175.
US2003087350-A1.
                                                                                                                                                       ADA61573 standard; protein; 660 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADA67523 standard; protein; 660 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 22.4%;
RESULT 815
                                        PD 20-MAR-2003,
PA (GETH) GENENTECH INC.
Query Match 10.2%;
Best Local Similarity 22.4%;
RESULT 812
                                                                                                                                                                                                                PD 13-MAR-2003.

PA (GETH ) GENENTECH INC.

QUETY MATCh

Best Local Similarity 22.4%;

RESULT 813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 10.2%;
Best Local Similarity 22.4%;
RESULT 816
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PA (GETH ) GENENTECH INC.

Query Match 10.2%;

Best Local Similarity 22.4%;

RESULT 817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-FEB-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity RESULT 819
                                                                                                                                                                            Homo sapiens.
US2003049816-A1.
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660;
                                                            Length 660;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 320; DB 6; Length 660;
Pred. No. 9.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.2%; Score 320; DB 6; Length 660; 22.4%; Pred. No. 9.3e-12;
                                                                                                                                                                                      Score 320; DB 6; Length 660;
Pred. No. 9.3e-12;
                                                                                                                                                                                                                                                                                                                  Score 320; DB 6; Length 660;
Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADA87481 standard; protein; 660 AA.
Novel human secreted and transmembrane protein PRO265.
US2003087345-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADA91775 standard; protein; 660 AA.
Novel human secreted and transmembrane protein PRO265.
                                                                                                                                                                                                                                                 Novel human secreted and transmembrane protein PRO265 US2003082693-A1.
                                                            Score 320; DB 6;
Pred. No. 9.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 320; DB 6;
Pred. No. 9.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 320; DB 6;
Pred. No. 9.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADA16064 standard; protein; 660 AA.
Human secreted/transmembrane protein, #7.
US2003049621-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human PRO polypeptide #175.
US2003087349-Al.
08-MAY-2003.
(GETH ) GENENTECH INC.
20.4%; Score 32
Next Match
10.2%; Pred. Nc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human PRO polypeptide #175.
01-Mav.
                                                                                                                                                                                                                                                                                                                                                             ADA97038 standard; protein; 660 AA.
Human PRO polypeptide #175.
US2003082705-A1.
(GETH ) GENENTECH INC.
                                                                                                      ADB30530 standard; protein; 660 AA.
Human PRO polypeptide #175.
US2003068794-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABO34821 standard; protein; 660 AA.
                                                                                                                                                                                                                                      protein; 660 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US2005vc.
01-MAY-2003.
(GETH ) GENENTECH INC.
Watch 10.2%; Sr
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13-MAR-2003.
(GETH ) GENENTECH INC.
10.2%;
                                                            10.2%;
22.4%;
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22.4%;
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22.4%;
Human PRO polypeptide #175
US2003068795-A1.
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US2003044793-A1.
06-MAR-2003.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Query Match
                                               (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                              Best Local Similarity RESULT 823
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RESULT 828
                                                                           Best Local Similarity
RESULT 821
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
RESULT 824
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                    ADA85826 standard;
                                10-APR-2003
                                                                                                                                                                                                                                                                                                                    Query Match
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Best Local
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RESULT Bast LC.
ID ADA85'
DE Nove
PN US'
PD '
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RESULT 825
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Length 660;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel human secreted and transmembrane protein PRO265.
US203082691-A1.
                                                                                                                                                                                                                                                                                                                                                                            Novel human secreted and transmembrane protein PRO265. US2003073211-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEGA3123 standard; protein; 660 AA.
Novel human secreted and transmembrane protein PRO265
US2003044945-A1.
                                                     10.2%; Score 320; DB 6; 22.4%; Pred. No. 9.3e-12;
                                                                                                                                                                                                                                           ADA47287 standard; protein; 660 AA.
Human secreted/transmembrane polypeptide PRO265
US2003044844-A1.
                                                                                                                                                                                                                                                                                                                                         Score 320; DB 6;
Pred. No. 9.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.2%; Score 320; DB 6; 22.4%; Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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                                                                                                                                                                                             Score 320; DB 6;
Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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Human secreted/transmembrane protein, #7.
US2003054401-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADA74476 standard; protein; 660 AA.
Human PRO polypeptide #175.
US2003068798-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADA94014 standard; protein; 660 AA.
Human PRO polypeptide #175.
US20030077722-AA.
24-APR-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADB13222 standard; protein; 660 AA.
Human PRO polypeptide #175.
US2003082710-A1.
                                                                                                          protein; 660 AA
                                                                                                                                                                                                                                                                                                                                         10.2%;
                                                                                                                                                                                             10.2%;
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Best Local Similarity 22.4%;
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Best Local Similarity 22.4%;
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Best Local Similarity 22.4%;
RESULT 835
                                                                                                                           Human PRO polypeptide #175
US2003087351-A1.
US2003082694-A1.
01-MAY-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                                                                                            08-MAY-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                     Best Local Similarity
                                                                                                          ADB14838 standard;
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                                                     Query Match
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                     Query Match
Best Local Similarity
RESULT 848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity RESULT 855
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                                                                                                                                                                       vuery Match
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 840
                                     Length 660;
                                                                                                                                                                                                                                                                                                                                         Length 660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 10.2%; Score 320; DB 6; Length 660; Best Local Similarity 22.4%; Pred. No. 9.3e-12; RESULT 844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.2%; Score 320; DB 6; Length 660; 22.4%; Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADA85274 standard; protein; 660 AA.
Novel human secreted and transmembrane protein PRO265.
US2003082695-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADA84722 standard; protein; 660 AA.
Novel human secreted and transmembrane protein PRO265.
US2003082708-A1.
                               Ouery Match
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 839
DE Human PRO polypeptide SEQ ID NO 350.
PD 24-APR-2003.
PD 42-APR-2003.
PD 42-APR-2003.
                                                                                                                                                                                                                                                                                                                                       Score 320; DB 6;
Pred. No. 9.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 10.2%; Score 320; DB 6; Best Local Similarity 22.4%; Pred. No. 9.3e-12; RESULT 843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 320; DB 6;
Pred. No. 9.3e-12;
                                                                                                                                                                                                                                           ADA82233 standard; protein; 660 AA.
Human PRO polypeptide #175.
US2003082701-A1.
                                                                                                                                                                                                                                                                                                                                                                                            ADA75196 standard; protein; 660 AA.
Human PRO polypeptide #175.
US2003073216-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABO17499 standard; protein; 660 AA. Human PRO polypeptide #6. US2003064367-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADB29978 standard; protein; 660 AA.
Human PRO polypeptide #175.
US2003073214-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADA80506 standard; protein; 660 AA.
Human PRO polypeptide #175.
US2003082761-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADA75748 standard; protein; 660 AA Human PRO polypeptide #175. 01-MAY-2003.
                                                                                                                                                                                                                                                                                                                                                                ...ard; protein;
...uard; protein;
...u3073216-A1.

17-APR-2003.

PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 22.4%; PrecREULT 842
ID ADA85274 standard; prrf
DE NOVEl human secret
PN US20030826°-
PA
                                                                                                                                                                                                                                                                                                  PD 01-MAY-2003.

PA (GETH) GENENTECH INC.

Query Match 10.2%;

Best Local Similarity 22.4%;

RESULT 841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 10.2%;
Best Local Similarity 22.4%;
RESULT 846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.2%;
                   GENENTECH INC.
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(GETH ) GENENTECH INC
Query Match
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(GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity RESULT 847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
20-MAR-2003
(GETH ) GEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-APR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 845
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Query Match 10.2%; Score 320; DB 6; Length 660; Best Local Similarity 22.4%; Pred. No. 9.3e-12; RESULT 851
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PN US200304917-A1.

PD 13-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 10.2%; Score 320; DB 6; Length 660; Best Local Similarity 22.4%; Pred. No. 9.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 320; DB 6; Length 660;
Pred. No. 9.3e-12;
                                                                                                                                                                        Length 660;
10.2%; Score 320; DB 6; Length 660; 22.4%; Pred. No. 9.3e-12;
                                                                                                                                                                                                                                                                                                                                         Length 660;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 660;
                                                                                                                                                                                                        ID AD25269 standard; protein; 660 AA.

DE Human PRO polypeptide SEQ ID NO 350.

PN US/2003077715-Al.

PD 24-APR-2003.

PA (GETH ) GENENTECH INC.

Query Match

Best Local Similarity 22.4%; Pred. No. 9.3e-12;

RESULT 850
                                                                                                        PD 17-APR-2003,
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 320; DB 6;
Pred. No. 9.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 320; DB 6;
Pred. No. 9.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 320; DB 6;
Pred. No. 9.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADB24157 standard; protein; 660 AA.
Human PRO polypeptide SEQ ID NO 350.
US2003077714-A1.
24-APR-2003.
(GETH ) GENENTECH INC.
24-BORT MATCH
10.24; SCORE 320
                                                          ADA46973 standard; protein; 660 AA.
Human PRO polypeptide #175.
US2003073210-A1.
                                                                                                                                                                                                                                                                                                                                                                                              ADM93445 standard, protein, 660 AA. Human PRO polypeptide #175. US2003007721-A1. 24-APR-2003. (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADB26795 standard; protein; 660 AA. Human PRO polypeptide #175. US2003092147-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADB31082 standard; protein; 660 AA.
Human PRO polypeptide #175.
US2003096386-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADA61010 standard; protein; 660 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADA96486 standard; protein; 660 AA.
Human PRO polypeptide #175.
US2003082690-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADA81058 standard; protein; 660 AA.
Human PRO polypeptide #175.
US2003082702-A1.
01-MAY-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PD 15-WAY-2003,
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 22.4%;
RESULT 852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PD 22-MAY-2003.

PA (GETH ) GENENTECH INC.

QUETY MATCh 10.2%;

BEST Local Similarity 22.4%;

RESULT 853
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Best Local Similarity 22.4%;
RESULT 856
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ADA86930 standard; protein; 660 AA.
Novel human secreted and transmembrane protein PRO265.
US2003082709-A1.
US2003082709-A1.
(OBTH ) GENENTECH INC.
ery Match
st Local Similarity 22.4%; Pred. No. 9.3e-12;
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(GETH ) GENENTECH INC.
10.2%; Score 320; DB 7; Length 660;
    Score 320; DB 6; Length 660;
Pred. No. 9.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 320; DB 7; Length 660; Pred. No. 9.3e-12;
                                                                                                                             Length 660;
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                                                                                                                                                                                                                                                                                        ADB21728 standard; protein; 660 AA.
Novel human secreted and transmembrane protein PRO265.
US2003082765-A1.
Ol-MAY-2003.
GETH ) GENENTECH INC.
ery Match
10.2%; Score 320; DB 6; Lengtl
st Local Similarity 22.4%; Pred. No. 9.3e-12;
                                                                                                                            Score 320; DB 6;
Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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US2003039969-A1.
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US2003049622-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADA1785 standard; protein; 660 AA.
Human secreted/transmembrane protein,
US2003082540-A1.
                                      Human PRO polypeptide #175.
US2003082759-A1.
                                                                                                                                                                     ADB26243 standard; protein; 660 AA.
Human PRO polypeptide #175.
US2003082760-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                   ADA77507 standard; protein; 660 AA.
Human PRO polypeptide #175.
US2003068797-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADB18247 standard; protein; 660 AA.
Human PRO polypeptide #175.
US2003077710-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADA16488 standard; protein; 660 AA
                                                                            US2003.cc.
01-MAY-2003.
(GETH ) GENENTECH INC.
werch 10.2%; Sc
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10-APR-2003.
(GETH ) GENENTECH INC.
March 10.2%; Sr
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01-MAY-2003.
(GETH ) GENENTECH INC.
MATCh '13-rity 22.48;
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22.4%;
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22.4%;
   10.2%;
22.4%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                         24-APR-2003.
(GETH ) GENENTECH INC.
Query Match
Best Local Similarity
RESULT 857
ID ADA95934 standard; p
DE Human PRO polypeptid
PN US2003082795-A1.
PD 01-WAY-2003.
PA (GETH) GENENTECH IN
                                                                                                                                                                                                                                                       Best Local Similarity
RESULT 859
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RESULT 860
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RESULT 863
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Best Local Similarity
RESULT 865
                                                                                                                          Query Match
Best Local Similarity
RESULT 858
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Best Local Si
RESULT 862
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Score 320; DB 7; Length 660; Pred. No. 9.3e-12;
                                                                                                                            Length 660;
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                                ADA88033 standard; protein; 660 AA.
Novel human secreted and transmembrane protein PRO265.
Novel human secreted and transmembrane protein PRO265.
OL-MAY-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                             numaeall standard; protein; 660 AA.
Novel human secreted and transmembrane protein PRO265.
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Novel human secreted and transmembrane protein PRO265.
US2003073213-A1.
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30-JAN-2003.

(GETH ) GENENTECH INC.

(GETH ) GENENTECH INC.

10.2%; SCORE 320; DB 7;

10.2%; SCORE 320; DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 320; DB 7;
Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
   22.4%; Pred. No. 9.3e-12;
                                                                                                                          Score 320; DB 7;
Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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Pred. No. 9.3e-12
                                                                                                                                                                                                                                                                                                             ADA17132 standard; protein; 660 AA.
Human secreted/transmembrane protein, #7.
US2003017498-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADA42635 standard; protein; 660 AA.
Human secreted/transmembrane protein, #7.
US2003054351-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADB29003 standard; protein; 660 AA.
Human PRO polypeptide #175.
US2003082706-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADA76955 standard; protein; 660 AA.
Human PRO polypeptide #175.
US2003059909-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADB28451 standard, protein, 660 AA-Human PRO polypeptide #175.
1052003082699-A1.
01-MAY-2003.
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                                                                                                                          10.2%;
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22.4%;
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RESULT 873
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22.4%;
                                                                                                                                                                                                                            20-MAR-2003.
(GETH ) GENENTECH INC.
Query Match
Best Local Similarity 22.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.2%;
22.4%;
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Human PRO polypeptide #175.
US200308266-A1.
01-MAY-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-APR-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GETH ) GENENTECH INC.
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                                                                                                                          Query Match
Best Local Similarity
Best Local Similarity RESULT 866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity RESULT 870
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Best Local Similarity
RESULT 869
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                  RESULT 868
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RESULT 874
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US2003082766-A1.
                                                                        Length 660;
                                                                                                                                                                      Length 660;
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Pred. No. 9.3e-12;
                                                                                                                                                                                                                                                                                     Length 660;
                                                                                                                                                                                                                                                                                                                                                                                                  10.2%; Score 320; DB 7; Length 660; 22.4%; Pred. No. 9.3e-12;
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                                                                                                             ADB22280 standard; protein; 660 AA.
Novel human secreted and transmembrane protein PRO265.
08-MAY-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADA92327 standard; protein; 660 AA.
Novel human secreted and transmembrane protein PRO265.
US2003082712-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADB38642 standard; protein; 660 AA.
Novel human secreted and transmembrane protein PRO265.
                                                                       Score 320; DB 7;
Pred. No. 9.3e-12;
                                                                                                                                                                                                                                                                                   10.2%; Score 320; DB 7; 22.4%; Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
                                                                                                                                                                                                         ABO19866 standard; protein; 660 AA.
Human secreted/transmembrane protein PRO265.
US2003044902-A1.
06-MAR-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADB23605 standard; protein; 660 AA. Human PRO polypeptide SEQ ID NO 350 US2003077712-A1.
RESULT 875

ID ADB27347 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN 105203032239-A1.
PD 30-JAN-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                         ADA66971 standard; protein; 660 AA. Human PRO polypeptide #175. US2003068793-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADB22832 standard; protein; 660 AA.
Human PRO polypeptide #175.
US2003077711-A1.
                                                                                                                                                                                                                                                                                                                              protein; 660 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADB15390 standard; protein; 660 AA. Human PRO polypeptide #175. US2003097352-A1. GB-MAY-2003. (GETH ) GENENTECH INC.
                                                                                                                                                                      10.2%;
                                                                       10.2%;
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RESULT 883
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22.4%;
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Human PRO polypeptide #6.
US2003064923-A1.
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(GETH ) GENENTECH INC.
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Query Match 1
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(GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                   (GETH ) GENENTECH INC
                                                                              Best Local Similarity
RESULT 876
ID ADB22280 standard; p
DE Novel human secreted
PN US2003087344-A1.
PD 08-MAY-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity RESULT 881
                                                                                                                                                                                                                                                                                            Best Local Similarity RESULT 878
                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity RESULT 879
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                                                                       Query Match
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RESULT 880
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Length 660;
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                                    Length 660;
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Novel human secreted and transmembrane protein PRO265.
US2003082764-A1.
(GETH ) GENENTECH INC.
                                                                                                      Novel human secreted and transmembrane protein PRO265 US200308747-A1.
08-MAY-2003 (GRTH ) GENENTECH INC.
                                                                                                                                                                                                                                 ADB66562 standard; protein; 660 AA.
Novel human secreted and transmembrane protein PRO265
US2003082689-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADB47098 standard; protein; 660 AA.
Novel human secreted and transmembrane protein PRO265.
US2003082687-A1.
                                    Score 320; DB 7;
Pred. No. 9.3e-12;
                                                                                                                                                                                                                                                                                                                              Score 320; DB 7;
Pred. No. 9.3e-12;
                                                                                                                                                                    Query Match 10.2%; Score 320; DB 7;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 886
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Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 320; DB 7;
Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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PA (GETH ) GENENTECH INC.

Query Match

10.2%; Score 320; DB

Best Local Similarity 22.4%; Pred. No. 9.3e-
RESULT 889

ID ADB77554 standard; protein; 660 AA.

DE Human secreted/transmembrane protein, #7.

PN US2003077654-A1.

PD 24-APR-2003.

PA (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADB74690 standard; protein; 660 AA.
Human secreted/transmembrane protein, #7.
US2003082542-A1.
                                                                                                                                                                                                                                                                                                                                                                        Human PRO polypeptide #175.
01-May A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADB90374 standard, protein, 660 AA.
Human PRO polypeptide #175.
US2003082762-A1.
                                                                                           660 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADB86705 standard; protein; 660 AA.
Human PRO polypeptide #175.
US2003082697-A1.
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01-MAY-2003.
(GETH ) GENENTECH INC.
"MATCh "Trity 22.4%;
PD 01-MAY-2003.

PA (GETH ) GENENTECH INC.

QUETY MATCh 10.2%;

BEST LOCAL Similarity 22.4%;

RESULT 885
                                                                                                                                                                                                                                                                                                                            10.2%;
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22.4%;
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RESULT 893
                                                                                           protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22.48;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC
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RESULT 891
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Best Local Similarity
RESULT 892
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Best Local Similarity
RESULT 887
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RESULT 890
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Best Local Similarity
RESULT 888
                                                                                       ADB38090 standard;
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24-AFK-2005. (GETH ) GENENTECH INC. ry Match 10.2%; Score 320; DB 7; Length 660; Length 660; Length 660; Length 660; Length 660 Length 660; Length 660; Length 660; Length 660; ADB77310 standard; protein; 660 AA. Novel human secreted and transmembrane protein PRO265 US2003082696-A1. ADB46518 standard; protein; 660 AA. Novel human secreted and transmembrane protein PRO265. US2003082692-A1. Ol-MAY-2003. (GETH ) GENENTECH INC. (GETH ) GENENTECH INC. 10.2%; Score 320; DB 7; ery Match 22.4%; Pred. No. 9.3e-12; US400-2... 24-APR-2003. (GFH) GENENTECH INC. (GFY) Match ery Match 10.2%; Score 320; DB 7; c.milarity 22.4%; Pred. No. 9.3e-12; ADB33915 standard; protein; 660 AA.

Human PRO polypeptide SEQ ID NO 350.
U\$2003077716-A1.
24-APR-2003.
(GEH ) GENENTECH INC.
ery Match
st Local Similarity 22.4%; Pred. No. 9.3e-12; 27-MAR-2003. (GETH) GENENTECH INC. (ery Match 10.2%; Score 320; DB 7; (ery Match 12.4%; Pred. No. 9.3e-12; Score 320; DB 7; Pred. No. 9.3e-12; 10.2%; Score 320; DB 7; 22.4%; Pred. No. 9.3e-12; Score 320; DB 7; Pred. No. 9.3e-12; Score 320; DB 7; Pred. No. 9.3e-12; ADC28336 standard; protein; 660 AA. Human secreted/transmembrane protein, #7. US2003059772-A1. ADC39536 standard; protein; 660 AA. Human secreted/transmembrane protein, #7. US2003059828-A1. 27-MAR-2003. ADB35571 standard; protein; 660 AA. Human PRO polypeptide SEQ ID NO 350. US2003077719-A1. Human PRO polypeptide SEQ ID NO 350. 1820037718-A1. Human PRO polypeptide SEQ ID NO 350. 1825003077720-A1. ADB34467 standard; protein; 660 AA. Human PRO polypeptide SEQ ID NO 350, US2003077717-A1. 24-APR-2003. U1-MAY-2003.

PA (GETH ) GENENTECH INC.

QUETY MALCH

BEST LOCAL Similarity 22.4%; Prer
RESULT 894

ID ADB77310 standard; probe Novel human secreting PN US20030826s PA US2005... 24-APR-2003. (GETH ) GENENTECH INC. Match 10.2%; US20050. 01-MAY-2003. (GETH ) GENENTECH INC. "MATCh 10.2%; 24-APR-2003. (GETH ) GENENTECH INC. Query Match Best Local Similarity RESULT 898 Query Match Best Local Similarity RESULT 895 Ouery Match Best Local Similarity RESULT 900 Query Match Best Local Similarity RESULT 897 Best Local Similarity RESULT 899 Best Local Similarity RESULT 901 Best Local Similarity RESULT 902 Query Match Query Match Query Match Query Match BERE

Score 320; DB 7; Length 660; Pred. No. 9.3e-12; Length 660; Score 320; DB 7; Pred. No. 9.3e-12; ADC34174 standard; protein; 660 AA.
Human secreted/transmembrane protein, #7.
US20030356094-A1.
20-FEB-2003.
(GETH ) GENENTECH INC.
ETY MATCh
St Local Similarity 22.4%; Pred. No. 9.3e-12; Human secreted/transmembrane protein, #7.
US2003049676-A1.
13-MAR-2003.
(GETH ) GENENTECH INC.
10.2%; Score 320; DB 7;
ELocal Similarity 22.4%; Pred. No. 9.3e-12; Score 320; DB 7; Pred. No. 9.3e-12; 10.2%; Score 320; DB 7; 22.4%; Pred. No. 9.3e-12; Score 320; DB 7; Pred. No. 9.3e-12; Score 320; DB 7; Pred. No. 9.3e-12; PD 13-MAR-2003.

PA (GETH ) GENENTECH INC.

Query Match

Best Local Similarity 22.4%; Pred. No. 9.

RESULT 908

ID ADC40645 standard; protein; 660 AA.

DIS Human secreted/transmembrane protein, #7.

PN US2003054400-A1. ADC19302 standard; protein; 660 AA. Human secreted/transmembrane protein, #7. 282003054441-A1. 20-MAR-2003. (GETH ) GENENTECH INC. Human secreted/transmembrane protein, #7 US2003059829-A1. ADC18878 standard; protein; 660 AA. Human secreted/transmembrane protein, #7 US2003036061-A1. Human secreted/transmembrane protein, #7. US2003049677-A1. ADC33750 standard; protein; 660 AA. Human secreted/transmembrane protein, #7. US2003073077-A1. ADC12820 standard; protein; 660 AA. Human secreted/transmembrane protein, #7 US2003073079-A1. ADC28760 standard; protein; 660 AA. ADC40050 standard; protein; 660 AA ADC29229 standard; protein; 660 AA (GETH ) GENENTECH INC. 10.2%; Sr ) 27-MAR-2003. A (GETH ) GENENTECH INC. Query Match 10.2%; Best Local Similarity 22.4%; 10.2%; Query Match 10.2%; Best Local Similarity 22.4%; Best Local Similarity 22.4%; RESULT 910 17-APR-2003. (GETH ) GENENTECH INC. 20-MAR-2003. (GETH ) GENENTECH INC. 17-APR-2003. (GETH ) GENENTECH INC. Query Match Best Local Similarity RESULT 903 Query Match Best Local Similarity RESULT 905 Best Local Similarity RESULT 906 Local Similarity Query Match Query Match Query Match Query Match Best Loc RESULT 904 RESULT 911

us-09-943-780-69.ragspdi

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Best Local Similarity 22.4%; Pred. No. 9.3e-12; RESULT 921
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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RESULT 925
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Best Local Similarity
RESULT 926
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Best Local Similarity
RESULT 923
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Best Local Similarity
RESULT 928
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(GETH ) GENENTECH INC.
10.2%; Score 320; DB 7; Length 660;
     Length 660;
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Novel human secreted and transmembrane protein Seg ID350.
US2003087365-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADC57278 standard; protein; 660 AA.
Novel human secreted and transmembrane protein Seq ID350.
US20030836-A1.
08-MAY-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADC54569 standard; protein; 660 AA.
Novel human secreted and transmembrane protein Seq ID350.
US2003087363-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADC60469 standard; protein; 660 AA.
Novel human secreted and transmembrane protein PRO265.
US2003087367-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADC50944 standard; protein; 660 AA.
Novel human secreted and transmembrane protein PRO265.
US2003087361-A1.
                                                    ADC50391 standard; protein; 660 AA.
Novel human secreted and transmembrane protein PRO265.
US2003092106-A1.
                                                                                                                                                                                         ADC71938 standard; protein; 660 AA.
Novel human secreted and transmembrane protein PRO265.
US2003092107-A1.
                                                                                                                                                                                                                                                                                                                                 ADC59917 standard; protein; 660 AA.
Novel human secreted and transmembrane protein PRO265.
US2003092105-A1.
   10.2%; Score 320; DB 7; 22.4%; Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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Human PRO polypeptide #175.
US2003087362-A1.
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22.4%;
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08-MAY-2003.
(GETH ) GENENTECH INC.
"ortch 10.2%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 916
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Best Local Similarity
RESULT 914
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Best Local Similarity
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Best Local Similarity
RESULT 918
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Best Local Similarity
RESULT 919
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                                                                                                                                                           Best Local Similarity
                   Local Similarity
                                                                                                          15-MAY-2003
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   Query Match
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                                     RESULT 912
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A D B B B B

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Query Match 10.2%; Score 320; DB 7; Length 660; Best Local Similarity 22.4%; Pred. No. 9.3e-12; RESULT.929
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Pred. No. 9.3e-12;
                                                                                                      Length 660
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ADC53530 standard; protein; 660 AA.
Novel human secreted and transmembrane protein Seg ID350.
US2003087364-A1.
08-MAY-2003.
                                                                                                                                                             ADC59053 standard; protein; 660 AA.
Novel human secreted and transmembrane protein Seg ID350.
US2003087359-A1.
                                                                                                                                                                                                                                                                                                                             ADC55931 standard; protein; 660 AA.
Novel human secreted and transmembrane protein Seg ID350
US2003087360-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADC56501 standard; protein; 660 AA.
Novel human secreted and transmembrane protein Seg ID350.
US2003087346-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADD03175 standard; protein; 660 AA.
Novel human secreted and transmembrane protein PRO265.
US2003092104-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADC90167 standard; protein; 660 AA.
Novel human secreted and transmembrane protein PRO265.
US2003087348-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADC12272 standard; protein; 660 AA.
Human secreted/transmembrane protein, #7.
US2003082541-A1.
01-MAY-2003.
(GETH) GENENTECH INC.
ery Match
10 24; Score 320; DB 7;
st Local Similarity 22.44; pred. No. 9.3e-12;
                                                             PA (GETH ) GENENTECH INC.

Query Match
10.2%; Score 320; DB 7;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 922
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PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 927
                                                                                                                                                                                                                                                                                                                                                                                                PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 320; DB 7;
Pred. No. 9.3e-12;
                                                                                                                                                                                                                                                                    Score 320; DB 7;
Pred. No. 9.3e-12;
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Human PRO polypeptide #175.
US2003194770-A1.
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08-MAY-2003.
(GETH ) GENENTECH INC.
watch 10.2%; S'
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RESULT 940
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RESULT 946
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                                                                                                                                                                                                                                                              Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADD10335 standard; protein; 660 AA.
Human secreted/transmembrane PRO polypeptide #23.
US2003105011-A1.
US2003105011-A1.
(GFTH ) GENENTECH INC.
ery Match
10.2%; Score 320; DB 7; Length 660;
st Local Similarity 22.4%; Pred. No. 9.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADC47923 standard; protein; 660 AA.

Human PRO polypeptide #175.

10-OCT-2003.

(GETH) GENENTECH INC.

11 0.2$; Score 320; DB 7; Length 660;

St Local Similarity 22.4$; Pred. No. 9.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.2%; Score 320; DB 7; Length 660; 22.4%; Pred. No. 9.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                           Score 320; DB 7; Length 660;
Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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                                                                                                                Length 660;
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                                                                                                                                                  AUUU4579 standard, protein, 660 AA.

Novel human secreted and transmembrane protein PRO265.
US2003087354-A1.
08-MAY-2003.
iry March
                                                                                                                                                                                                                                                                                                Novel human secreted and transmembrane protein PRO265
US203092103-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADC79983 standard; protein; 660 AA. Novel human secreted and transmembrane protein PRO265 US2003087358-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 22.4%; Pred. No. 9.3e-12; RESULT 938
D. Albalos standard; protein; 660 AA. DE Human secreted/transmembrane PRO polypeptide #23.0 No. 9.30310513-A1.
PD 05-2107-2003.
PA (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.2%; Score 320; DB 7; 22.4%; Pred. No. 9.3e-12;
                                                                                                            Score 320; DB 7;
Pred. No. 9.3e-12;
                                                                                                                                                                                                                                                              Score 320; DB 7;
Pred. No. 9.3e-12;
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Pred. No. 9.3e-12
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Human secreted/transmembrane protein, #7.
US2003104469-A1.
               ADD10004 standard; protein; 660 AA. Human PRO polypeptide #175. US2003194776-Al. 16-OCT-2003. (GET) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADD11042 standard; protein; 660 AA.
Human PRO polypeptide #175.
US2003194774-Al.
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(GETH ) GENENTECH INC.
Watch
Total 10.2%; Sf
                                                                                                            10.2%;
22.4%;
                                                                                                                                                                                                                                                          10.2%;
22.4%;
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1S-MAY-2003.
(GETH ) GENENTECH INC.
MARCh '...itv 28;
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16-OCT-2003.
(GETH ) GENENTECH INC.
10.2%;
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                                                                                                                                                                                                                                                                        Best Local Similarity
RESULT 932
ID ADG80535 standard; pr
DE Novel human secreted
PN US2003092103-A1.
PD 15-MAY-2003
PA (GETH ) GENENTECH INC
RESULT 930

ID ADD10004 standard; p
DE Human PRO polypeptid
PN US2003194776-A1.
PD 16-CCT-2003.
PA (GETH ) GENENTECH IN
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                                                                                                                           Best Local Similarity RESULT 931
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
RESULT 933
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Best Local Similarity
RESULT 939
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RESULT 936
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Score 320; DB 7; Length 660;
Pred. No. 9.3e-12;
                                                                                    Length 660;
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US200320348-A1.
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Novel human secreted and transmembrane protein PRO265.
US2003203437-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADD37088 standard; protein; 660 AA.
Human secreted/transmembrane PRO polypeptide #23
US2003105012-A1.
                                                                                                                                                                                                                                                                                                                                                                  10.2%; Score 320; DB 7; 22.4%; Pred. No. 9.3e-12;
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(GETH ) GENENTECH INC.
10.2%; Score 320; DB 7;
Lery Match 12:4%; Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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                                                                                     Score 320; DB 7;
Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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US2003109893-A1.
                                                                                                                                  ADD03833 standard; protein; 660 AA.
Human secreted/transmembrane protein, #7.
US2003104381-A1.
05-JUN-2003.
(GETH ) GENENTECH INC.
10.2%; Score 320;
st Local Similarity 22.4%; Pred. No. 9.
ADD09452 standard; protein; 660 AA.
Human PRO polypeptide #175.
US2003194775-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADD53044 standard; protein; 660 AA.
Human PRO polypeptide #175.
US2003194792-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADD52304 standard; protein; 660 AA. Human PRO polypeptide #175. US2003194769-A1.
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22.4%;
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Query Match
Best Local Similarity 22.4%;
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Best Local Similarity 22.4%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                    (GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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Best Local Similarity
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Best Local Similarity
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US2003194772-A1.
                                                              Length 660;
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Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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                                                                                                                                                                                                                        ADD54167 standard; protein; 660 AA.
Novel human secreted and transmembrane protein PRO265.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADE32291 standard; protein; 660 AA.
Novel human secreted and transmembrane protein PRO265.
US2003194765-A1.
                                                            Score 320; DB 7;
Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
                                                                                                                                                                                   Score 320; DB 7;
Pred. No. 9.3e-12;
                                                                                                                                                                                                                                                                                                            Score 320; DB 7;
Pred. No. 9.3e-12;
                                                                                                      ADD01985 standard; protein; 660 AA.
Human PRO polypeptide #175.
US2003203430-A1.
                                                                                                                                                                                                                                                                                                                                                     ADD92484 standard; protein; 660 AA.
Human PRO polypeptide #175.
US2003199030-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADD91380 standard; protein; 660 AA.
Human PRO polypeptide #175.
US2003199055-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADE03994 standard, protein, 660 AA.
Human PRO polypeptide #175.
US2003199057-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADE22223 standard; protein; 660 AA.
Human PRO polypeptide #175.
US2003199056-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADE41983 standard; protein; 660 AA
Human PRO polypeptide #175.
                                                                                                                                                                                                                                                             US2001203.
30-OCT-2003.
(GETH ) GENENTECH INC.
10.2%;
                           30-0cT-2003.
(GETH ) GENENTECH INC.
10.2%;
ory Match 10.2%;
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22.4%;
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                                                                                                                                              PD 30-OCT-2003.

PA (GETH ) GENENTECH INC.

Query Match

Best Local Similarity 22.4%;

RESULT 950
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22.4%;
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Human PRO polypeptide #175.
US2003203428-A1.
Human PRO polypeptide #175.
US2003203431-A1.
30-OCT-2003.
      2003.
2003.
2003.
21-A1.
2003.
2ery Match
Best Local Similarity 2
RESULT 949
ID ADD01985 standa-
DE Human PRO r.
PN US20032.
PD 30-
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(GETH ) GENENTECH INC.
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JS-A1.

LM JGENENTECH 1

LM JGENENTECH 1

LM BEST Local Similarity 1

RESULT 953

ID ADE03994 stand 2

DE Human PRO 7

PN US200317

PD 23-7

PA
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC
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Best Local Similarity
RESULT 956
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
RESULT 952
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Best Local Similarity
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Best Local S
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Best Local S
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PD 16-OCT-2003.

PA (GETH) GENENTECH INC.

Query Match

10.2%; Score 320; DB 7; Length 660;

Best Local Similarity 22.4%; Pred. No. 9.3e-12;

RESULT 962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADD93036 standard; protein; 660 AA.

Human PRO polypeptide #175.

1 US2003194768-A1.

16-OCT-2003.

Query Match

Best Local Similarity 22.4%; Pred. No. 9.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 660;
                                 10.2%; Score 320; DB 7; Length 660; 22.4%; Pred. No. 9.3e-12;
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US2003194767-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADE33947 standard; protein; 660 AA.
Novel human secreted and transmembrane protein PRO265.
US2003194791-A1.
                                                                                                                                                                           Score 320; DB 7;
Pred. No. 9.3e-12;
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Query Match
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 966
                                                                                                                                                                                                                                                                                                                        Score 320; DB 7;
Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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                                                                                 ADE17800 standard; protein; 660 AA.
Human PRO polypeptide #175.
23-203199023-A1.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                             ADD91912 standard; protein; 660 AA.
Human PRO polypeptide #175.
US2003199053-A1.
C3-OCT-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADD79999 standard; protein; 660 AA.
Human PRO polypeptide #175.
US2003207417-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADE19456 standard; protein; 660 AA.
Human PRO polypeptide #175.
US2003199025-A1.
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                                                                                                                                                                       Best Local Similarity 22.4%;
RESULT 959
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PA (GETH ) GENENTECH INC.
Query March
Best Local Similarity 22.4%;
RESULT 961
                                                                                                                                                                                                                                                                                                                    Query Match 10.2%;
Best Local Similarity 22.4%;
RESULT 960
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22.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 22.4%;
RESULT 964
16-OCT-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-OCT-2003.
(GETH ) GENENTECH INC.
                                              Best Local Similarity
RESULT 958
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                                   Query Match
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(GETH ) GENENTECH INC.
                             Score 320; DB 7; Length 660;
Pred. No. 9.3e-12;
                                                                                                                                                                                                                                                                    Length 660;
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Pred. No. 9.3e-12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADE32843 standard; protein; 660 AA.
Novel human secreted and transmembrane protein PRO265.
US2003194766-A1.
16-OCT-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                Score 320; DB 7;
Pred. No. 9.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                    Score 320; DB 7;
Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
                                                                      ADE43100 standard; protein; 660 AA. Human PRO Polypeptide #175. US2003199033-A1. 23-OCT-2003. GENENTECH INC. 10.2%; Score 32 pery Match 10.2%; Score 32 est Local Similarity 22.4%; Pred. No.
                                                                                                                                                                                         ADD95889 standard; protein; 660 AA.
Human PRO polypeptide #175.
US2003199059-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADE22775 standard; protein; 660 AA.
Human PRO polypeptide #175.
US2003199064-A1.
C33-OCT--2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                             ADD78893 standard; protein; 660 AA.
Human PRO polypeptide #175.
US2003203499-A1.
30-OCT-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADD89579 standard; protein; 660 AA.
Human PRO polypeptide #175.
US2003199028-A1.
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Human PRO polypeptide #175.
US2003207418-A1.
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Human PRO polypeptide #175.
US2003199031-A1.
33-OCT-2003.
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06-NOV-2003.
(GETH ) GENENTECH INC.
...Match 10.2%; SC
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23-OCT-2003.
(GETH ) GENENTECH INC.
"arch 'lrity 22,4%;
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CGETH ) GENENTECH INC.
ATCh | 10.2%;
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RESULT 969
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                           Match 10.2%;
Local Similarity 22.4%;
                                                                                                                                                                                                                                  23-OCT-2003.
(GETH ) GENENTECH INC.
23-OCT-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
RESULT 971
ID ADB32843 standard; pr
DE Novel human secreted
PN US2003194766-A1.
PD 16-OCT-2003
PA (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
RESULT 970
ID ADD78893 standard, p.
DE Human PRO polypeptid
PN US2003203429-A1.
PD 30-CCT-2003.
PA (GETH ) GENENTECH IN
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Best Local Similarity
RESULT 973
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Best Local Similarity
RESULT 974
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                                             Best Loca
RESULT 967
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Score 320; DB 7; Length 660; Pred. No. 9.3e-12;
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 Length 660;
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                                                                                                                                                                                                                                                                                                                                ADG21500 standard; protein; 660 AA.
Novel human secreted and transmembrane protein PRO265.
US2003207355-A1.
06-NOV-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADG23141 standard; protein; 660 AA.
Novel human secreted and transmembrane protein PRO265
US2003207384-A1.
 Score 320; DB 7;
Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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                                                                                                                                                                                                                                                                                10.2%; Score 320; DB 7; 22.4%; Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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Pred. No. 9.3e-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human PRO polypeptide #175.
US2003207372-A1.
06-NOV-2003.
                                                ADE04662 standard; protein; 660 AA.
Human PRO polypeptide #175.
US2003199034-AA.
23-OCT-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                         ADE92791 standard; protein; 660 AA.
Human PRO polypeptide #175.
US2003194777-A1.
16-OCT-2003.
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Human PRO polypeptide #175.
US2003207370-A1.
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                                                                                                                                   Best Local Similarity 22.4%;
RESULT 977
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22.4%;
Query Match 10.2%;
Best Local Similarity 22.4%;
RESULT 976
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Query Match 10.2%;
Best Local Similarity 22.4%;
RESULT 983
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Best Local Similarity 22.4%;
RESULT 984
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Best Local Similarity 22.4%;
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Human PRO polypeptide #175.
US2003207373-A1.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                            Best Local Similarity RESULT 978
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Best Local Similarity
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RESULT 980
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Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 994
      Length 660;
                                                                                                                                       Length 660;
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Pred. No. 9.3e-12;
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A (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
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                                              ADH55280 standard; protein; 660 AA.
Novel human secreted and transmembrane protein PRO265.
05-003207381-A1.
06-NOV-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                               ADH55832 standard; protein; 660 AA.
Novel human secreted and transmembrane protein PRO265.
US2003207379-A1.
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Novel human secreted and transmembrane protein PRO265.
US2003207386-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADI65499 standard; protein; 660 AA.
Novel human secreted and transmembrane protein PRO265.
US2003207387-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADH81913 standard; protein; 660 AA.
Novel human secreted and transmembrane protein PRO265.
US2003207388-A1.
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Novel human secreted and transmembrane protein PRO265.
US2003207377-A1.
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Novel human secreted and transmembrane protein PRO265.
US2003087355-A1.
 10.2%; Score 320; DB 7; 22.4%; Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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Human secreted/transmembrane protein, #7.
US2003054352-A1.
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Human secreted/transmembrane protein, #7
                                                                                                                                    10.2%;
22.4%;
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22.4%;
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RESULT 991
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22.4%;
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Best Local Similarity 22.4%;
RESULT 990
                                                                                                                                                                                                                                  06-NOV-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 989
ID AD163499 standard; pro
DE Novel human secreted by US20032073487-A1.
PD 06-NOV-2003.
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                                                                                                                           Query Match
Best Local Similarity
RESULT 986
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 Query Match
Best Local Similarity
RESULT 985
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Score 320; DB 8; Length 660; Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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ID ADM15929 standard; protein; 660 AA.

DE Novel human secreted and transmembrane protein PRO265.

PN US2003087353-A1.

PD 08-MAY-2003.

PA (GETH) GENENTECH INC.

Query Match

Best Local Similarity 22.4%; Pred. No. 9.3e-12;

RESULT 995
                                                                                                                                 ADN16558 standard; protein; 660 AA.
Novel human secreted and transmembrane protein PRO265
                                                                                                                                                                                                                                                     ADNIS377 standard; protein; 660 AA.
Novel human secreted and transmembrane protein PRO265
US2003087356-A1.
                                                                                                                                                                                                                                                                                                                                                                                ADN14825 standard; protein; 660 AA.
Novel human secreted and transmembrane protein PRO265 US2003087357-A1.
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Novel human secreted and transmembrane protein PRO265
US2003207385-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADC81087 standard; protein; 660 AA.
Novel human secreted and transmembrane protein PRO265 US2003092115-A1.
                                                                                                                                                                                                             Score 320; DB 7;
Pred. No. 9.3e-12;
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PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 999
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Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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Pred. No. 9.3e-12
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Human secreted/transmembrane protein, #7.
US2003135025-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         660 AA
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15-MAY-2003.
(GETH ) GENENTECH INC.
10.2%; SC
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08-MAY-2003.
(GETH ) GENENTECH INC.
10.2%; S.
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17-JUL-2003.
(GETH ) GENENTECH INC.
"arch 10.2%; Sr
                                                                                                                                                                                                                                                                                                          ra (GETH) GENENTECH INC.
Query Match
Best Local Similarity 22.4%;
RESULT 997
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PA (GETH ) GENENTECH INC.

QUETY MATCh 10.2%;

Best Local Similarity 22.4%;

RESULT 1002.
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 998
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Best Local Similarity
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Best Local Similarity
RESULT 1001
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Score 320; DB 8; Length 660; Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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Human secreted/transmembrane PRO polypeptide #23.
US2003100497-A1.
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Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
                                                                                                                                                                                                                                                                                                                                                                  Score 320; DB 8;
Pred. No. 9.3e-12;
                                                                                                                                                                Human secreted/transmembrane protein, #7.
US2003130489-A1.
10-JUL-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                  #2
                                                                                                                                                                                                                                                                                                                                                                                                              ADE73206 standard; protein; 660 AA.
Human secreted/transmembrane protein,
US2003129592-A1.
RESULT 1003

ID ADD86303 standard; protein; 660 AA.

DE Human RRO polypeptide #175.

PN US2003203404-A1.

PD 30-OCT-2003.

PA (GETH ) GENENTECH INC.

Query Match

Ouery Match

10.2%; Score 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADE23327 standard; protein; 660 AA.
Human PRO polypeptide #175.
US2903092108-A1.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human PRO polypeptide #175.
US2003092110-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADE24522 standard, protein, 660 AA.
Human PRO polypeptide #175.
US2003092111-A1.
                                                                                                                                                                                                                                                                               ADE75'51 standard; protein; 660 AA.
Human PRO polypeptide #175.
US2003211571-A1.
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JAD087347 standard; protein; 660 AA.
Human PRO polypeptide #175.
US2003203439-A1.
                                                                                                                                                    ADE79530 standard; protein; 660 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   USZUCZZO
10-7UL-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US2003.
15-MAY-2003.
(GETH ) GENENTECH INC.
MARCH 10.2%;
                                                                                                                                                                                                                                10.2%;
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13-NOV-2003.
(GETH ) GENENTECH INC.
Match 10.2%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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LIH ) GENENTECH .

LY MAICH BEST LOCAL SIMILARILY .

RESULT 1008
ID ADE23327 standa .

DE Human PRO .

PN US20030 .

PD 15 .
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Best Local Similarity
RESULT 1009
ID ADE22879 standard; pr
DE Human PRO polypeptide
PN US2003092110-A1.
PD 15-WAY-2003
PA (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
RESULT 1010
DE ADE24522 standard; p.
DE Human PRO polypeptid
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH IN
                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
RESULT 1006
ID ADE73206 standard; p
DE Human secreted/trans
pN US20312952-A1.
PD 10-JUL-2003.
PA (GETH ) GENENTECH IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
RESULT 1011
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Best Local Similarity
RESULT 1007
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Best Local Similarity
RESULT 1012
                                                                                                                   Best Local Similarity RESULT 1004
                                                                                                                                                                                                                                             Best Local Similarity
RESULT 1005
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23-OCT-2003.
(GETH) GENENTECH INC.
ery Match 10.2%; Score 320; DB 8; Length 660;
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Pred. No. 9.3e-12;
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                                                                               Length 660;
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                                                                                                     Score 320; DB 8;
Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
                                                                               Score 320; DB 8;
Pred. No. 9.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADE99295 standard; protein; 660 AA.
Human secreted/transmembrane protein, #7.
102003211576-A1.
13-NOV-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                    ADE73741 standard; protein; 660 AA.
Human secreted/transmembrane protein, #7
US2003148370-A1.
                                                                                                                                                                                                                                                                                                                                                                       Human PRO polypeptide #175.
ADE89213 standard; protein; 660 AA.
Human PRO polypeptide #175.
US2003199062-A1.
C3-OCT-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADE91092 standard; protein; 660 AA.
Human PRO polypeptide #175.
US2003199061-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JAE88661 standard; protein; 660 AA.
Human PRO polypeptide #175.
US2003199054-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADE94681 standard; protein; 660 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADE93343 standard; protein; 660 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             660 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local older Personal RESULT 1020
ID ADE95233 standard; protein; 66
DE Human PRO polypeptide #175.
PN US2003199052-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DE Human PRO polypeptide #175.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 22.4%;
RESULT 1019
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                                                                          Best Local Similarity 22.4%;
RESULT 1013
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22.4%;
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Best Local Similarity 22.4%;
                                                                                                                                                                                                                                                                                            PD 07-AUG-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%;
Best Local Similarity 22.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                            PD 16-OCT-2003.

PA (GETH ) GENENTECH INC.

QUETY MATCh 10.2%;

Best Local Similarity 22.4%;

RESULT 1016
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity RESULT 1017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity RESULT 1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Length 660;

Length 660;

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vuery Match
Best Local Similarity 22.4%; Score 320; DB 8; Length 660;
RESULT 103.2
ID ADG20122 standard; protein; 660 AA.
PN US2003207376-A1.
PN US2003207376-A1.
PA O FOLYPEPTIGE #175.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vuery Match 10.2%; Score 320; DB 8; Length 660; Best Local Similarity 22.4%; Pred. No. 9.3e-12; RESULT 1033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 10.2%; Score 320; DB 8; Length 660; Best Local Similarity 22.4%; Pred. No. 9.3e-12; RESULT 1038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 320; DB 8; Length 660;
Pred. No. 9.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.2%; Score 320; DB 8; Length 660; 22.4%; Pred. No. 9.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADG24245 standard; protein; 660 AA.
Novel human secreted and transmembrane protein PRO265.
US2003207426-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DD 06-NOV-2003.

PD 06-NOV-2003.

PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity 22.4%; Pred. No. 9.3e-12;

RESULT 1034

ID ADG24245 standard; protein; 660 AA.

BN Novel human secreted and tran-
PN US2003207426-AI.

PD 06-NOV-2003.
                                                                              10.2%; Score 320; DB 8; 22.4%; Pred. No. 9.3e-12;
                                                                                                                                                                                                                           Score 320; DB 8;
Pred. No. 9.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 320; DB 8;
Pred. No. 9.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                               AUGU122 standard; protein; 660 AA. Human PRO polypeptide #175. US2003207376-A1. 06-NOV-2003. GTH) GENENTECH INC.
                                                                                                                                ADG02266 standard, protein; 660 AA.
Human PRO polypeptide #175.
US2003207352-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADF98599 standard; protein; 660 AA.
Human PRO polypeptide #175.
US2003208055-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADG03430 standard, protein, 660 AA.
Human PRO polypeptide #175.
US2003207351-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADF99151 standard, protein, 660 AA.
Human PRO polypeptide #175.
US2003207353-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADG16736 standard; protein; 660 AA.
Human PRO polypeptide #175.
US2003207359-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US200240...
06-NOV-2003.
(GETH ) GENENTECH INC.
...watch 10.2%; Sr
                                                                                                                                                                                                                       Match 10.2%;
Local Similarity 22.4%;
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PA (GETH ) GENENTECH INC.

QUETY MATCh 10.2*;

BEST LOCAL SIMILATITY 22.4*;

RESULT 1036
                                                             (GETH ) GENENTECH INC.
                                                                                                                                                                                                        (GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                           Best Local Similarity RESULT 1030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
RESULT 1037
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Best Local Similarity
RESULT 1035
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                                                                                                                        PD 23-OCT-2003

PA (GETH) GENENTECH INC.

Query Match

BEST LOCal Similarity 22.4%; Pred. No. 9.3e-12;

RESULT 1023

ID ADE98414 standard; protein; 660 AA.

PD WINAM SECRET PROTEIN; 660 AA.

PD 13-NOV-2003

PD 13-NOV-2003

PA (GETH) GENENTECH INC.

10.2%; Score 320; DB 8; Length 660; RESULT 1023

PD ADE98414 standard; protein; 660 AA.

PD 13-NOV-2003

PD 13-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                        Length 660;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADE92239 standard; protein; 660 AA.
Novel human secreted and transmembrane protein PRO265.
US2003199051-A1.
32-OCT-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1026
ID ADE91687 standard; protein; 660 AA.
BN US200319908-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
LOUST 99060-A1.

PD 23-OCT-2003.

PA (GETH) GENENTECH INC.

Query Match

Best Local Similarity 22.4%; Pred. No. 9.3e-12;

RESULT 1022

ID ADF34924 standard; protein; 660 AA.

BE Human PRO polypeptide #175.

PD 33-OCT-2007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 22.4%; Score 320; DB 8; BESULT 10.7 10 ADB9841 standard; protein; 660 AA.

DE Human secreted/transmembrane protein, #7.

PN US2003211568.A1.

PD 13-NOV-2003.

PA (GETH ) CENTENT ...
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Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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Human secreted/transmembrane protein, #7
US2003225253-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADF73705 standard; protein; 660 AA.
Human secreted/transmembrane protein, #7.
25208-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADE90540 standard, protein, 660 AA.
Human PRO polypeptide #175.
US2003199063-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                     10.2%;
22.4%;
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22.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (DESN/) DESNOYERS L. (GODC/) GODDARD A. (GODC/) GODOWSKI P J. (GURN/) GURNEY A L. (WALLI/) MATLLIAMS P M. (WOOD/) WOOD W I.
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2003.

2003.

A.H.) GENENTECH I.

Jry Match
Best Local Similarity 2.

RESULT 1024

ID ADE22239 standar

DE Novel humar

PN US2031"

PD 23-
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 1028
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Best Local Similarity
RESULT 1025
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(GETH ) GEN
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Best Loca. RESULT 1029

Length 660;

Length 660

Length 660;

Length 660;

Length 660;

Length 660;

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Score 320; DB 8; Length 660; Pred. No. 9.3e-12;
                                                                                                                                                                                                                     Novel human secreted and transmembrane protein PRO265.
US2032207427-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel human secreted and transmembrane protein PRO265. US200207428-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                 ADG07180 standard; protein; 660 AA.
Novel human secreted and transmembrane protein PRO265.
US2003207350-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADG55227 standard; protein; 660 AA.
Novel human secreted and transmembrane protein PRO265.
US2003194778-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADG66891 standard; protein; 660 AA.
Novel human secreted and transmembrane protein PRO265 US2003207390-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADG07732 standard; protein; 660 AA.
Novel human secreted and transmembrane protein PRO265
US2003207356-A1.
                                                                                                                                                                   Score 320; DB 8;
Pred. No. 9.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 320; DB 8;
Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
Best Local Similarity 22.4%; Fred. No. 9.3e-12; RESULT 1048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-NOV-2003.

(GETH ) GENENTECH INC.

(GETH ) GENENTECH INC.

10.2%; Score 320; DB 8;

lery Match
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Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADG03982 standard; protein; 660 AA.
Human PRO polypeptide #175.
US2003207423-A1.
GGFTH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein; 660 AA
                                                                                                                                                                     10.2%;
22.4%;
                                                                                                                                                                                                                                                                                                  PD 06-NOV-2003.

PA (GETH ) GENENTECH INC.

QUETY MATCh 10.2%;

Best Local Similarity 22.4%;

RESULT 1050
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22.4%;
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Best Local Similarity 22.4%;
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Best Local Similarity 22.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human PRO polypeptide #175
US2003207358-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-WOV-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-FEB-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-NOV-2003.
(GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENENTECH INC
                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity RESULT 1056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity RESULT 1052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
RESULT 1054
ID ADG61995 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADG82196 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-NOV-2003
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                                                                                                                                                                        Query Match
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                                                                                                                                                                                             Best Loca
RESULT 1049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 1053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 320; DB 8; Length 660; Pred. No. 9.3e-12;
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(GETH ) GENENTECH INC.
10.2%; Score 320; DB 8; Length 660;
         Length 660;
                                                                                                                                                                                                                                                                                                                                                                               Length 660;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADG08356 standard; protein; 660 AA.
Novel human secreted and transmembrane protein PRO265.
US2003207424-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADG22693 standard; protein; 660 AA.
Novel human secreted and transmembrane protein PRO265.
US2003207389-A1.
       Score 320; DB 8;
Pred. No. 9.3e-12;
                                                                                                                                                                                                                                                                                                                                                                               Score 320; DB 8;
Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
                                                                                                                                                                                           Score 320; DB 8;
Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                ADF73281 standard; protein; 660 AA.
Human secreted/transmembrane protein, #7.
04-SEP-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human PRO polypeptide #175.
US2003207371-A1.
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US2003207374-A1.
                                                                                                                                                                                                                                                         AGG19462 standard; protein; 660 AA.
Human PRO polypeptide #175.
US2003207425-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADG13299 standard; protein; 660 AA.
Human PRO polypeptide #175.
US2003207357-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADG15526 standard, protein, 660 AA.
Human PRO polypeptide #175.
US2003219885-A1.
                                                                            protein; 660 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US200512.
04-SEP-2003.
(GETH ) GENENTECH INC.
"11ch 10.2%; Sr
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06-NOV-2003.
(GETH ) GENENTECH INC.
10.2%; SC
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06-NOV-2003.
(GETH ) GENENTECH INC.
Match 'Trity 22.4%;
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06-NOV-2003.
(GETH ) GENENTECH INC.
Match '128;
       10.2%;
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(GETH ) GENENTECH INC.
20ery Match 10.2%;
20ery The control of the c
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                                                                     ADGG5195 standard; protein;
Human PRO polypeptide #175.
US2003207375-Al.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LAT.

LOO3.

LY MATCH

BEST LOCAL SIMILARITY

RESULT 1042

D AD013299 stande

DE Human PRO

PN US20032

PD 06-7
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RESULT 1045
ID ADF96924 standard; pz
DE Human PRO polypeptide
PN US2003207311-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
RESULT 1041
ID ADF73281 standard, pl
DE Human secreted/transm
PD 04-SEP-2003.
PA (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
RESULT 1047
ID ADG23693 standard; p
DE Novel human secreted
PN US2003207389-A1.
PD 06-NOV-2003.
Query Match
Best Local Similarity
RESULT 1039
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RESULT 1043
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1044
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Best Local Similarity
RESULT 1040
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RESULT 1046
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Best Local Si
RESULT 1044
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Length 660;

Length 660;

Length 660;

Query Match

Query Match

Length 660;

Score 320; DB 8; Length 660; Pred. No. 9.3e-12;

Length 660;

Score 320; DB 8; Pred. No. 9.3e-12;

Length 660;

Score 320; DB 8; Pred. No. 9.3e-12;

Length 660;

Length 660

Length 660;

Length 660;

Score 320; DB 8; Pred. No. 9.3e-12;

Best Loca RESULT 1064

A D S E D

us-09-943-780-69.ragspdi

RESULT 1057
ID ADG5743
DE Novel h
PN US20032
PD 06-NOV-

A B S E B

PDNE

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ADG$4123 standard; protein; 660 AA.

Novel human secreted and transmembrane protein PRO265.
US2003207416-A1.
06-NOV-2003.
(GETH ) GENENTECH INC.
10.2%; Score 320; DB 8; Length
st Local Similarity 22.4%; Pred. No. 9.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                 ADHI1973 standard; protein; 660 AA.
Novel human secreted and transmembrane protein PRO265.
US2003207419-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADG52395 standard; protein; 660 AA.
Novel human secreted and transmembrane protein PRO265
US2003207414-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADG56331 standard; protein; 660 AA.
Novel human secreted and transmembrane protein PRO265.
US2003207366-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADH12597 standard; protein; 660 AA.
Novel human secreted and transmembrane protein PRO265
US2003207378-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADG61443 standard; protein; 660 AA. Novel human secreted and transmembrane protein PRO265
                                                                                                                                                                                                                                                                             ADG6345 standard; protein; 660 AA.
Human secreted/transmembrane polypeptide PRO265.
US2003180796-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-NOV-2003.
(GETH) GENENTECH INC.
ery Match 10.2%; Score 320; DB 8;
ery Match 22.4%; Pred. No. 9.3e-12;
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PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1070
ADG81644 standard; protein; 660 AA.
Human PRO polypeptide #175.
US2003207805-A1.
06-NOV-2003.
                                                                                                                            ADH30606 standard; protein; 660 AA.
Human PRO polypeptide #175.
US2003077723-A1.
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Human PRO polypeptide #175.
US2003194793-A1.
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06-NOV-2003.
(GETH ) GENENTECH INC.
10.2%; Sr
                                                                           10.2%;
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PA (GETH ) GENENTECH INC.

QUETY MATCh

Best Local Similarity 22.4%;

RESULT 1068
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(GETH ) GENENTECH INC.
10.2%;
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(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
RESULT 1071
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                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity RESULT 1069
                                                                                           Best Local Similarity
RESULT 1067
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RESULT 1075
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Pred. No. 9.3e-12;
                                                                                                                                                                                                                                                              Length 660;
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           ADG57435 standard; protein; 660 AA.
Novel human secreted and transmembrane protein PRO265.
US2003207362-A1.
                                                                                                                                                           ADGS6883 standard; protein; 660 AA.
Novel human secreted and transmembrane protein PRO265.
US2003207364-A1.
                                                                                                                                                                                                                                                                                                                ADG55779 standard; protein; 660 AA.

Novel human secreted and transmembrane protein PRO265.
US2003207365-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADGS8539 standard; protein; 660 AA.
Novel human secreted and transmembrane protein PRO265.
US2003207368-AI.
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Novel human secreted and transmembrane protein PRO265.
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Novel human secreted and transmembrane protein PRO265.
US2003207353-A1.
06-NOV-2003.
(GETH ) GENENTECH INC.
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US2003207415-A1.
06-NOV-2003.
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Novel human secreted and transmembrane protein PRO265.
US2003207421-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 320; DB 8;
Pred. No. 9.3e-12;
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Pred. No. 9.3e-12;
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                                                                                                            Score 320; DB 8;
Pred. No. 9.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                               Score 320; DB 8;
Pred. No. 9.3e-12;
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ID ADG92551 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
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Best Local Similarity 22.4%;
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(GETH ) GENENTECH INC.
                                                                     06-NOV-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                          (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
RESULT 1059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity RESULT 1061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity RESULT 1063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                        Best Local Similarity RESULT 1058
                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity RESULT 1060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US2003027146-A1.
                                                                                                                                                                                                                       06-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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A D M E D

S S S S S

Length 660;

Score 320; DB 8; Pred. No. 9.3e-12

Length 660;

Score 320; DB 8; Pred. No. 9.3e-12;

Score 320; DB 8; Length 660; Pred. No. 9.3e-12;

Length 660;

Score 320; DB 8; Pred. No. 9.3e-12;

Score 320; DB 8; Length 660; Pred. No. 9.3e-12;

Query Match

Query Match

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OJ-AUG-2003.
(GETH ) GENENTECH INC.
(ery Match 10.2%; Score 320; DB 8; Length 660;
ery Match 22.4%; Pred. No. 9.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 10.2%; Score 320; DB 8; Length 660; Local Similarity 22.4%; Pred. No. 9.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 10.2%; Score 320; DB 8; Length 660; Local Similarity 22.4%; Pred. No. 9.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 1090
ID ADI15353 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
PA (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADG09230 standard; protein; 660 AA.
Novel human secreted and transmembrane protein PRO265.
US2004009547-A1.
15-JAN.2004.
(GEUH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADG09882 standard; protein; 660 AA.
Novel human secreted and transmembrane protein PRO265
US2004009548-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human secreted/transmembrane protein, #7.

N US2003096340-A1.

O 22-MAX-2003.

A (GETH ) GENENTECH INC.

Query Match

Dest Local Similarity 22.4%; Pred. No. 9.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                               PD 14-AUG-2003.

PA (GETH ) GENENTECH INC.

Query Match
Best Local Similarity 22.4%; Pred. No. 9.

RESULT 1086

ID AD165230 standard; protein; 660 AA.

BUS2003148419-A1.
                                                                                                                                                                                                                                                                                                                                                  ADI18510 standard; protein; 660 AA.
Human secreted/transmembrane protein, #7
US2003152999-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADF97297 standard; protein; 660 AA.
Human secreted/transmembrane protein, #7.
US2003190610-A1.
                                                                                                                                                                                    ADIBILI39 standard; protein; 660 AA.
Human PRO polypeptide #175.
US2003207361-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADI37493 standard; protein; 660 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 10.2%;
Best Local Similarity 22.4%;
RESULT 1092
                                                                                                                            10.2%;
22.4%;
                                                                                                                                                                                                                                               PD 06-NOV-2003.

PA (GETH ) GENENTECH INC.

QUETY MATCh 10.2%;

BBSL Local Similarity 22.4%;

RESULT 1085
(GODD/) GODDARD A. (GODO/) GODOWSKI P J. (GURN/) GURNEY A L. (MAILL) MILLILAMS P M. (WICL) WILLILAMS P M. (WOOD/) WOOD W I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JAN-2004.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-OCT-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity RESULT 1087
                                                                                                                       Query Match
Best Local Similarity
RESULT 1084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loca
RESULT 1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OG-NOV-2003.
(GETH ) GENENTECH INC.
ery Match 10.2%; Score 320; DB 8; Length 660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-DEC-2003.
(GETH ) GENENTECH INC.
ery Match 10.2%; Score 320; DB 8; Length 660;
                                                                   Length 660;
                                                                                                                                                                                                                            Length 660;
                                                                                                                                                                                                                                                                                                                                                                                            10.2%; Score 320; DB 8; Length 660; 22.4%; Pred. No. 9.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 320; DB 8; Length 660; Pred. No. 9.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 320; DB 8; Length 660;
Pred. No. 9.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.2%; Score 320; DB 8; Length 660; 22.4%; Pred. No. 9.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                    المحتمدة (AA. Novel human secreted and transmembrane protein PRO265 US2003200307369-A1.
                                                                                                                                                                                                                                                                                   ADGS4675 standard, protein, 660 AA.
Novel human secreted and transmembrane protein PRO265
US2003207367-A1.
06-NOV2-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                               Best Local Similarity 22.4%; Score 320; DB 8; BestLocal Similarity 22.4%; Pred. No. 9.3e-12; RESULT 1077

ID ADGS4675 standard; protein; 660 AA.

DE Novel human secreted and transmembrane protein PP No 092003207367A1.

PD 06-NOV-2003.

PA (GETH ) CENDENTALL
                                                             10.2%; Score 320; DB 8; 22.4%; Pred. No. 9.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human secreted/transmembrane protein, #7.
US2004005553-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADH07195 standard; protein; 660 AA.
Human secreted/transmembrane protein, #7
US2004006211-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADH06768 standard; protein; 660 AA.
Human secreted/transmembrane protein, #7.
220040056567-A1.
08-JAN-2004.
(DESN/) DESNOYERS I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 22.4%; Pred. No.
RESULT 1082.
DD AD459740 standard; protein; 660 AA.
DE Human secreted/transmembrane protein; 400 20-00V-2003.
DR GETH ) GENENTECH INC.
                                                                                                                     ADH28530 standard; protein; 660 AA.
Human PRO polypeptide #175.
US200302231.A1.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AD43479 standard; protein; 660 AA. Human PRO polypeptide #23. US2003224984-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADH20340 standard; protein; 660 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 22.4%;
RESULT 1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-JAN-2004.
(GDEN/) DESNOYERS I.
(GODD/) GODDARD A.
(GOND/) GODOWSKI P J.
(GURN/) GURNEY A I.
(WALH) MATHER J P.
(WILL/) WILLIAMS P M.
(WOOD/) WOOD W I.
                         06-NOV-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JAY.

2003.

2003.

FY Match
Best Local Similarity
RESULT 1083
ID ADH06768 stand-
DE Human secre
PN US20040.
PD 08-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
RESULT 1079
ID ADH20340 standard; pi
DE Human secreted/trans
PN US2004005553-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity RESULT 1078
                                                                 Query Match
Best Local Similarity
RESULT 1076
      US2003207429-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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Length 660;

Score 320; DB 8; Length 660; Pred. No. 9.3e-12;

Length 660;

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PD 04-MAR-2004.

PA (GETH ) GENENTECH INC.

Query Match 10.2%; Score 320; DB 8; Length 660; Best Local Similarity 22.4%; Pred. No. 9.3e-12; RESULT 1102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-FEB-2004.
(GETH ) GENENTECH INC.
ery Match 10.24; Score 320; DB 8; Length 660;
                                     Score 320; DB 8; Length 660; Pred. No. 9.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660; Best Local Similarity 22.4%; Fred. No. 9.3e-12; RESULT 1105
                                                                                                                                                                                                                                                                                                                              Score 320; DB 8; Length 660;
Pred. No. 9.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PD 15-JUL-2004.

PA (GETH ) GENENTECH INC.

QUENTY MATCh 10.2%; Score 320; DB 8;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 320; DB 8;
Pred. No. 9.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 320; DB 8;
Pred. No. 9.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADRI0915 standard; protein; 660 AA.
Human secreted/transmembrane protein, #7.
US2004137561-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADR17824 standard; protein; 660 AA.
Human secreted/transmembrane protein, #7
US2004147017-A1.
                                                                                                                                                                                                                            DE Human PRO polypeptide #175.

PN US2004038335-A1.

PD 26-FEB-2004.

PA (GETH ) GENENTECH INC.

Query Match

Best Local Similarity 22.4%; Pred. No.
               PA (GETH ) GENENTECH INC.

Query Match
10.2%; Score
Best Local Similarity 22.4%; Pred.
RESULT 1101
ID ADK82824 standard; protein; 660 AA.
DE Human PRO polypeptide #23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADM28300 standard; protein; 660 AA.
Human PRO polypeptide #175.
US2004077064_A1.
22-APR-2004.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                 ADM27714 standard; protein; 660 AA.
Human PRO polypeptide #175.
US2004048333-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADM42438 standard; protein; 660 AA.
Human PRO polypeptide #175.
US2004058424-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AD006063 standard; protein; 660 AA.
Human PRO polypeptide #6.
US6686451-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
QUETY MATCh 10.2%;
Best Local Similarity 22.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 22.4%;
RESULT 1106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.2%;
22.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DESNOYERS L.
EATON D L.
FERRARA N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILVAROFF E. FONG S. GAO W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ASHK/) ASHKENAZI A. (BOTS/) BOTSTEIN D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity RESULT 1107
     26-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (FILV/)
(FONG/)
(GAOW/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (DESN/)
(EATO/)
(FERR/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DAPAPADAED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GETH ) GENENTECH INC.

Query Match

Best Local Similarity 22.4%; Pred. No. 9.3e-12;

RESULT 1099

ID ADM29741 standard; protein; 660 AA.

PN US2003190611-A1.

PD 09-OCT-20^^
                                                                                                                                                                                                                                                                                                                                               Length 660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.2%; Score 320; DB 8; Length 660; 22.4%; Pred. No. 9.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vuery Match
10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1098
                                                                                          Length 660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 320; DB 8; Length 660;
Pred. No. 9.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.2%; Score 320; DB 8; Length 660; 22.4%; Pred. No. 9.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 660;
ADI14685 standard; protein; 660 AA.
Novel human secreted and transmembrane protein PRO265.
US2003207383-A1.
                                                                                                                                                                                                                                                                                                                                                                                                ADII8280 standard; protein; 660 AA.
Novel human secreted and transmembrane protein PRO265.
US2003207349-A1.
                                                    PD 06-NOV-2003.

PA (GETH) GENENTECH INC.

Query Match

10.2%; Score 320; DB 8;

Beet Local Similarity 22.4%; Pred. No. 9.3e-12;

RESULT 1093
                                                                                                                                                                                                                                                                                                                                                 Score 320; DB 8;
Pred. No. 9.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.2%; Score 320; DB 8; 22.4%; Pred. No. 9.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADL08650 standard; protein; 660 AA.
Human secreted/transmembrane protein, #7.
022003106358-A1.
02-0CT-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADM24995 standard; protein; 660 AA.
Human secreted/transmembrane protein, #7.
US2003096233-A1.
                                                                                                                                         ADH60400 standard; protein; 660 AA.
Human secreted/transmembrane protein, #7.
US2004023331-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADJ99457 standard; protein; 660 AA.
Human secreted/transmembrane protein, #7.
US2003187238-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADJ77456 standard; protein; 660 AA.
Human PRO polypeptide #175.
US2004038336-A1.
                                                                                                                                                                                                                                                                                                                                                 10.2%;
22.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 22.4%;
RESULT 1100
                                                                                                                                                                                                05-FEB-2004.
(GDD/) GDDDARD A.
(GDD/) GDDDARD A.
(GDD/) GURNEX P J.
(GURN/) GURNEY A L.
(MATH) MATHER J P.
(WILL/) WILLIAMS P M.
(WOOD/) WOOD W I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-NOV-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O 02-OCT-2003.
GETH ) GENENTECH INC.
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) 22-MAY-2003.
A (GETH ) GENENTECH INC.
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity RESULT 1095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity RESULT 1096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
RESULT 1097
                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
RESULT 1094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Length 660;

Length 660;

Length 660;

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A (WOOD/) WG
A (ZHAN/) Zi
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (DEFO/)
(DESN/)
(FILV/)
(GAOW/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SHER/)
(SMIT/)
(STEW/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TUMA/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (WATA/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADI36334 standard, protein, 660 AA.

Novel human secreted and transmembrane protein PRO265.

N US2003207354-A1.

N 06-NOV-2003.

A (GETH ) GENENTECH INC.

Query Match

Best Local Similarity 22.4%; Pred. No. 9.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.2%; Score 320; DB 8; Length 660; 22.4%; Pred. No. 9.3e-12;
                                                                                                                                             Score 320; DB 8; Length 660;
Pred. No. 9.3e-12;
                                                                                                                                                                                                                                                                                                                                                                 Length 660;
                                                                                                                                                                                                                  10.2%; Score 320; DB 8; Length 660; 22.4%; Pred. No. 9.3e-12;
                                                                                                                                                                                                                                                                                                                                                             Query Match 10.2%; Score 320; DB 8; Best Local Similarity 22.4%; Pred. No. 9.3e-12; RESULT 1112
                                                                                                                                                                                                                                                                                                                   ADI65657 standard; protein; 660 AA.
Human secreted/transmembrane protein, #7.
US2003148371-A1.
                                                                                                                                                                                                                                                                                                                                                                                         ADS74463 standard; protein; 660 AA.
Human secreted/transmembrane protein #7.
US2004185531-A1.
                                                                                                                                                                      ADI95782 standard; protein; 660 AA.
Human PRO polypeptide #175.
US2003077659-A1.
                                                                                                                                             10.2%;
22.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GODOWSKI P J.
GRIMALDI C J.
GURNEY A L.
HILLAN K. J.
KLJAVIN I J.
MATHER J P.
PAN J.
PAONI N F.
ROY M A.
STEWART T A.
TUMAS D.
WILLIAMS P M.
                GODDARD A.
GODOWSKI P J.
GRIMALDI C J.
GURNEY A L.
HILLAN K J.
                                                                                                                                                                                                24-APR-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                              07-AUG-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GERBER H.
GERRITSEN M E.
                                                           KLJAVIN I J.
MATHER J P.
PAN J.
PAONI N F.
ROY M A.
STEWART T A.
TUMAS D.
WILLIAMS P M.
GERBER H.
GERRITSEN M E.
                                                                                                                                                                                                                                                                                                                                                                                                                           ASHKENAZI A.
BOTSTEIN D.
DESNOYERS L.
EATON D L.
FERRARA N.
FILVAROFF E.
FONG S.
                                                                                                                                                                                                                Query Match
Best Local Similarity
RESULT 1110
                                                                                                                                                    Best Local Similarity RESULT 1109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GODDARD A.
                                                                                                                                                                                                                                                                                                                                                                                                                     23-SEP-2004.
(ASHK/) ASHH
(BOTS/) BOTS
(DESN/) DESN
                                                                                                                                             Query Match
                                                                                                                  (TUMA/)
(WILL/)
(WOOD/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (WILL/)
                                                                                        (PAON/)
(ROYM/)
(STEW/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (FERR/)
                        (GODO/)
(GRIM/)
(GURN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (FONG/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (PANJ/)
(PAON/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TUMA/
                                                    (HILL/)
(KLJA/)
(MATH/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (KLJA/)
(MATH/)
                                                                               (PANJ)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STEW/
                                                                                                                                                                                                                                                                                                           RESULT 1111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GERB/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GERR/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GODO/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GRIM/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GURN/
                 GODD/
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7 1119
AEB14067 standard; protein; 660 AA.
Cancer cell diagnosis method-related human protein - SEQ ID 350.
US2005153396-Al.
                                                                                                                                                                                                                                                                                 vuery Match 10.2%; Score 320; DB 8; Length 660; Best Local Similarity 22.4%; Pred. No. 9.3e-12; RESULT 1115
                                                                                                                                Length 660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.2%; Score 320; DB 9; Length 660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADU06386 standard; protein; 660 AA.

Novel bronchial cancer-associated human protein SegID610.
DE10316701-A1.
04 NOV-2004.
(HINZ/) HINZMANN B.
(HERM/) HERMANN K.
(CAST/) HEIDEN CASTANOS-VELEZ B.
RESULT 1113

ID ADS32286 standard; protein; 660 AA.

ID ADS32286 standard; protein; 660 AA.

IO Novel human secreted and transmembrane protein PRO265.

PN US2004203125-A1.

PD 14-0CT-2004.

PA (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1118
ID AEA37738 standard; protein; 660 AA.
BY HUST 1128
ID AEA37758 standard; protein; 670 AA.
BY HUMAN Secreted/transmembrane protein, #7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 10.2%; Score 320; DB 9;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1119
                                                                                                                     uuery Match
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.2%; Score 320; DB 8; 22.4%; Pred. No. 9.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 320; DB 8;
Pred. No. 9.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADZ03321 standard; protein; 660 AA.
Human secreted/transmembrane PRO265 protein.
US2005074837-A1.
                                                                                                                                                                                                                                                                                                                                                                                       Human secreted/transmembrane protein, #7
US2003152922-A1.
                                                                                                                                                                                           ADT03270 standard, protein, 660 AA.
Human PRO polypeptide #175.
US2004214259-A1.
28-OCT-2004.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                     ADT03500 standard; protein; 660 AA.
                                                                                                                                                                                                                                                                                                                                                                                                             PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%;
Best Local Similarity 22.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-APR-2005.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-MAY-2005.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GODOWSKI P J.
GURNEY A L.
SHERWOOD S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GERRITSEN M E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMITH V.
STEWART T A.
TUMAS D.
WATANABE C K.
WOOD W I.
ZHANG Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BAKE/) BAKER K P.
(BERE/) BERESINI M.
(DEFO/) DEPORGE L.
(DESN/) DESNOYERS L.
(FILV/) FILVAROFF E.
(GAOW/) GAO W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
RESULT 1117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GODDARD A.
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10.0%; Score 314.5; DB 8; Length 474;

AAUJ1341 standard; protein, 656 AA.

DE Human novel secreted protein LP223(b).

PN W0200214358-A2.

PA (ELIL) LILLY & CO ELI.

Query Match

Best Local Similarity 23.6%; Pred. No. 2.4e-11;

RESULT 1128

ID ADL24097 standard; protein, 713 AA.

DE Human NOWY polypeptide #71.

PN US2004002120-A1.

PA (KERU/) FERUDA PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PD 21-OCT-2004.

PA (UYRP) UNIV ROCHESTER.

Query Match
Best Local Similarity 27.8%; Pred. No. 7.5e-12;
RESULT 1122

ID AAE13006 standard; protein; 713 AA.

DE Human leucine-rich repeat (LRR) family member protein.

PN W0200175105-A2.

PD 11-OCT-2001.

PA (WILL-) MILLENNIUM PHARM INC.

Query Match
Best Local Similarity 23.1%; Pred. No. 1.5e-11;

RESULT 1123

ID AAU91335 standard; protein; 713 AA.

DE Human novel secreted protein LP223(a).

PN W0200214358-A2.

PN W0200214358-A2.
                                                                                                                                                                                                                                                                                   Best Local Similarity 27.3%; Score 318.5; DB 8; Length 452; RESULT 1121

ID ADT77802 standard; protein; 452 AA.

DE Chimeric Nogo receptor polypeptide.

PN W02004090103-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D ABG7791 standard; protein; 713 AA.

DB Human nervous system leucine rich repeat protein (HLRRNS1) #2.

PN W0200274959-A2.

PD 26-SEP-2002.

PA (BRIM ) BRISTOL-MYERS SQUIBB CO.

Query Match

10.1%; Score 316.5; DB 5; Length 713;

Best Local Similarity 23.1%; Pred. No. 1.7e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 10.1%; Score 316.5; DB 5; Length 713; Best Local Similarity 23.1%; Pred. No. 1.7e-11; RESULT 1124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 10.1%; Score 316.5; DB 6; Length 713; Best Local Similarity 23.1%; Pred. No. 1.7e-11; RESULT 1126
           22.4%; Pred. No. 9.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABUS2381 standard; protein; 713 AA. Human GPCR related protein NOV31a. WO200279398-A2.
                                                                                                     ADT77808 standard; protein; 452 AA. Chimeric Nogo receptor polypeptide. WOZO04090103-A2. 21-OCT-2004. (UYRP.) UNIV ROCHESTER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADT77796 standard; protein; 474 AA.
Chimeric Nogo receptor polypeptide.
WO2004090103-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-OCT-2002.
(CURA-) CURAGEN CORP.
Best Local Similarity RESULT 1120
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DB 8; Length 713;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
10.0%; Score 312; DB 4; Length 592;
Best Local Similarity 25.9%; Pred. No. 2.6e-11;
RESULT 1130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 10.0%; Score 312; DB 5; Length 592; Beet Local Similarity 25.9%; Pred. No. 2.6e-11; RESULT 1131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 10.0%; Score 312; DB 5; Length 592; Best Local Similarity 25.9%; Pred. No. 2.6e-11; RESULT 1132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.0%; Score 312; DB 5; Length 592; 25.9%; Pred. No. 2.6e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU79167 standard; protein; 592 AA.
Human leucine-rich repeat proteins-like protein NOV4.
WO200214368-A2.
21-FEB-2002 (CURA.) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 23.1%; Pred. No. 2.6e-11;
RESULT 1129
AAE09437 standard; protein; 592 AA.
DE Human sbgTango79a protein.
PN W0200160850-A1.
PD A3-AUG-2001.
PA (SMIX ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU91329 standard; protein; 592 AA.
Human novel secreted protein LP243(b).
WO200214358-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE25351 standard; protein; 592 AA. Human LP polypeptide, LP243. WO200248361-A2. CO-JUN-2002. (ELIL ) LILLY & CO ELI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-AUG-2001.
(SMIK ) SMITHKLINE BEECHAM CORP.
(SMIK ) SMITHKLINE BEECHAM PLC. SCOT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-JUN-2002.
(SMIK ) SMITHKLINE BEECHAM CORP.
(SMIK ) SMITHKLINE BEECHAM PLC.
(GLAX ) GLAXO GROUP LTD.
                                                                                                                                                                                                                                                                                                                                                                              (RAST) RASTELLI L. (SPAD) SPADERNA S K. (LARO) LAROCHELLE W J. (ZHOM) ZHONG M. (KHRA) KHRAMTSOV N V. (VOSS) VOSS E Z. (HERR) HERRMANN J L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-FEB-2002.
(ELIL) LILLY & CO ELI.
                                                             GOLMAN L.
MALYANKAR U M.
BOLDOG F L.
GUO X.
SHENOY S G.
PADIERR W.
TAUPIER C B.
CASMAN S J.
PERICE C B.
CASMAN S J.
PERICE C B.
CASMAN S J.
PENA C B A.
GANGOLLI E A.
GUSEV V Y.
SMITHSON G.
PATTURAJAN M.
BURGESS C E.
VERNET C A M.
                                                                                                                                                                                                                                                                                                                                                   FERNANDES E R
                                                                                                                                                                                                                                                                                                                                                                       SHIMKETS R A.
                                                                                                                                                                                                                                                                                                               GERLACH V. POCHART P F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity RESULT 1133
(PATT/)
(BURG/)
(VERN/)
                                                  (LILL/)
(GORM/)
(MALY/)
(BOLD/)
(GUOX/)
                                                                                                                                                        (PADI/)
(TAUP/)
(MILL/)
(CASM/)
                                                                                                                                                                                                                                                                                                                (GERL/)
(POCH/)
                                                                                                                                                                                                                                                               (GOSE/)
                                                                                                                                                                                                                                                                                                                                                                     (/WIHS)
                                                                                                                                                                                                                                                                                                ZERH/
                                                                                                                                                                                                                                                                                                                                                   (FERN/
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Query Match 9.9%; Score 310.5; DB 6; Length 674; Best Local Similarity 21.5%; Pred. No. 3.8e-11; RESULT 1142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 6; Length 420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 24.1%; Pred. No. 3.3e-11;
RESULT 1139

ID ARR55628 standard; protein; 420 AA.
DE Amino acid sequence of rat Nogo-66 receptor homologue NgRH1.
PD 01-MAY-2003
PA (NOVS ) NOVARTIS AG.
PA (NOVS ) NOVARTIS PHARMA GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    O4-NOV-2004.

(FIVE-) FIVE PRIME THERAPEUTICS INC.

(FIVE-) FIVE PRIME THERAPEUTICS INC.

ery Match

10.0%; Score 312; DB 8; Length 592;

ery Match

25.9%; Pred. No. 2.6e-11;
  Score 312; DB 5; Length 592;
Pred. No. 2.6e-11;
                                                                                                                                                                                                                                                                                                                                                                                                         10.0%; Score 312; DB 7; Length 592; 25.9%; Pred. No. 2.6e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG97967 standard; protein; 634 AA.
Human nervous system leucine rich repeat protein (HLRRNS1)
26-SEP-2002.
(BRIM ) BRISTOL-MYERS SQUIBB CO.
ery Match
9.9%; Score 311; DB 5; Length 634;
                                                                                                                                                                  Length 592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 310.5; DB 8;
Pred. No. 2.2e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 29.8%; Pred. No. 2.2e-11; RESULT_1140
                                                                                                            MV2.0-2-3.
20-FED 2003.
(INCY-) INCYTE GENOMICS INC.
ery Match
10.0%; Score 312; DB 6;
ery Match
10.0%; Pred. No. 2.6e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 312; DB 5;
Pred. No. 2.7e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAO23115 standard; protein; 674 AA.
FLRT1 'human modifier of p53 pathway' protein.
WO2003035833-A2.
                                                                                                                                                                                                                      ADE03417 standard; protein; 592 AA.
Human immunoglobulin superfamily member BGS-2.
US2003195163-A1.
                                             Human CGDD protein; 592 AA.
Human CGDD protein 6803363CD1 SEQ ID 19.
                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 25.9%; Pred. RESULT 1136
DE ADUO2709 standard; protein; 592 AA. DE Novel human polypeptide seqid 1176. PN W02004093804-A2. PD G-NOV-2004.
PD (FIVE-) FIVE PRIME THERAPEUTICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABG61770 standard; protein; 608 AA.
Novel leucine-rich protein.
WO200229058-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADT77788 standard; protein; 420 AA.
Rat Nogo receptor 2 polypeptide.
WO2004090103-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADH17606 standard; protein; 674 AA.
    10.0%;
25.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.0%;
25.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-OCT-2004.
(UYRP ) UNIV ROCHESTER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-APR-2002.
(CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2003.
(EXEL-) EXELIXIS INC.
                                                                                                                                                                                                                                                                                16-OCT-2003.
(WUSS/) WU S.
(KRYS/) KRYSTEK S R.
(LEEL/) LEE L.
(FEDE/) FEDER J N.
(CHEN/) CHENG J D.
Query Match
Best Local Similarity
REGULT 1134
ID ABG74693 standard; pi
DE Human CGDD protein 6(
PN W02003014922-A2.
PD 20-FEB-2003.
PA (INCY-) INCYTE GENOM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
RESULT 1137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
RESULT 1138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                          Ouery Match
Best Local Similarity
RESULT 1135
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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RESULT 1141
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Length 674;
                                                                         DB 8; Length 674;
                                                                                                                                                                                                                                                                                                                                                                  Length 674;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 8; Length 674;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 674;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 22.3%; Score 309; DB 6; Length 585; RESULT 1149

ID AAU29215 standard; protein; 649 AA.

DE Human PRO POLypeptide sequence #192.

PN W0200166848-A2.

PD 20-SEP-2001.

PA (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 309; DB 6; Length 585; Pred. No. 4e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.9%; Score 309; DB 4; Length 649; 22.3%; Pred. No. 4.6e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 649;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABO34232 standard; protein; 585 AA.
Human secreted/transmembrane polypeptide PRO 1865.
US2003060601-A1.
                                                                                                                                                                                                                                                                                                                                                                   Query Match 9.9%; Score 310.5; DB 8;
Best Local Similarity 21.5%; Pred. No. 3.8e-11;
                                                                                                                                                                                                                       DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 1147
ID ABO27346 standard; protein; 585 AA.
DE Human secreted/transmembrane polypeptide PRO1865.
PN US2003009012-A1.
                                                                         9.9%; Score 310.5; DB 8, 21.5%; Pred. No. 3.8e-11;
                                                                                                                                                                                                                     9.9%; Score 310.5; DB 8, 21.5%; Pred. No. 3.8e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                y Match 9.9%; Score 310.5; DB 8. Local Similarity 21.5%; Pred. No. 3.8e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 310.5; DB 8;
Pred. No. 3.8e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 309; DB 4;
Pred. No. 4.6e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human PRO3 protein; 649 AA. WO200110902-A2. FEBE 2001.
                                                                                                                           ADH17628 standard; protein; 674 AA.
Human NOV191 protein - SEQ ID 318.
WO2003093432-AZ.
                                                                                                                                                                                                                                                         RESULT 1144
ID ADH17630 standard; protein; 674 AA.
DE Human NOV19m protein - SEQ ID 320.
PN WO20030993432-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADH17632 standard; protein; 674 AA.
Human NOV19n protein - SEQ ID 322.
MO2003093432-A2.
13-NOV-2003.
(CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 1145
ID ADH17634 standard; protein; 674 AA.
DE Human NOV190 protein - SEQ ID 324.
PN W02003093432-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB87591 standard; protein; 649 AA
Human PRO1865.
Human NOV19a protein - SEQ ID 296.
WO2003093432-A2.
13-NOV-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 22.3%;
RESULT 1148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-JAN-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-MAR-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-NOV-2003.
(CURA-) CURAGEN CORP.
                                                                                                                                                                                 13-NOV-2003.
(CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                              13-NOV-2003.
(CURA-) CURAGEN CORP.
                                                        (CURA-) CURAGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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RESULT 1150
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Best Local Similarity
RESULT 1151
                                                                                                                                                                                                                                       Local Similarity
                                                                                     Best Local Similarity RESULT 1143
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                                                                         Query Match
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RESULT 1159
                                         Length 649;
                                                                                                                                                    Length 649;
                                                                                                                                                                                                                                                              Score 309; DB 5; Length 649;
Pred. No. 4.6e-11;
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Pred. No. 4.6e-11;
                                                                                                                                                                                                                                                                                                                                                                           Length 649;
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                                                                                                                                                                                                                                                                                                                                                                                                              ABB95559 standard; protein; 649 AA.
Human angiogenesis related protein PRO1865 SEQ ID NO: 274.
WO200208284-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABU88139 standard; protein; 649 AA.
Novel human secreted and transmembrane protein PRO1865.
US2003032127-A1.
13-FEB-2003.
                                      9.9%; Score 309; DB 4; 22.3%; Pred. No. 4.6e-11;
                                                                                                                                           Lucry match 9.9%; Score 309; DB 5; Best Local Similarity 22.3%; Pred. No. 4.6e-11; RESULT 1153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 309; DB 5;
Pred. No. 4.6e-11;
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Pred. No. 4.6e-11;
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Human secreted/transmembrane protein (PRO) #192.

US2003023112-A1.

13-FEB-2003.

Query Match

Query Match
                                                                                                                                                                                                                                                                                                                                                                         9.9%; Score 309; DB 5; 22.3%; Pred. No. 4.6e-11;
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Pred. No. 4.6e-11;
                                                                                             Human secreted/transmembrane protein PRO1865.
US2002119130-A1.
                                                                                                                                                                                        ABB84953 standard; protein; 649 AA.
Human PRO1865 protein sequence SEQ ID NO:274.
WO200200690-A2.
                                                                                                                                                                                                                                                                                                  ABP70109 standard; protein; 649 AA.
Human NOV27a.
WO200272771-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABU58591 standard; protein; 649 AA.
Human PRO polypeptide #192.
US2003027272-A1.
                                                                                649 AA
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Local Similarity 22.3%;
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                                                                                protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GODO/) GODOWSKI P J.
(GURN) GURNEY A L.
(HILL) HILLLAN K J.
(MARS/) MARSTERS S A.
(PANN/) PAN J.
(PANN/) PAONI N F.
(STEV/) STEPHAN J F.
(WATLA/) WATANABE C K.
(WILL)/ WILLLIAMS P M.
(WOOD/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GERBER H.
GERRITSEN M E.
GODDARD A.
                                                                                                                                                                                                                                 03-JAN-2002.
(GETH ) GENENTECH INC.
           08-MAR-2001.
(GETH ) GENENTECH INC.
                                                                                                                        29-AUG-2002.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                               19-SEP-2002.
(CURA-) CURAGEN CORP.
                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity RESULT 1155
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Best Local Similarity
RESULT 1156
                                                                  T 1152
ABG95916 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BAKE/) BAKER K P. (FERR/) FERRARA N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity RESULT 1157
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WO200116318-A2.
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                                        Query Match
                                                                                                                                                                                                                                                              Query Match
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(GERR/)
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(GODO/)
(GURN/)
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Score 309; DB 6; Length 649; Pred. No. 4.6e-11;
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                                                                                                                                                                                                                                                                                                                                                                                             Novel human secreted and transmembrane protein PRO1865-20-303036147-A1.
ABR66328 standard; protein; 649 AA.
Human secreted polypeptide PRO1865, SEQ ID NO:384.
US2003027278-A1.
                                                                               Human secreted polypeptide PRO1865, SEQ ID NO:384. US2003036159-A1.
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Human secreted polypeptide PR01865, SEQ ID NO:384
                                                                                                                                                                                             אס אפספבים, protein; 649 AA.
Human secreted/transmembrane protein (PRO) #192.
US20030040070-A1.
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US2003044923-A1.
06-MAR-2003.
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Human secreted/transmembrane protein (PRO) #192.
US2003036149-A1.
20-FEB-2003.
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US2003040062-A1.
27-FEB-2003.
                                                       Score 309; DB 6;
Pred. No. 4.6e-11;
                                                                                                                                                               Score 309; DB 6;
Pred. No. 4.6e-11;
                                                                                                                                                                                                                                                                                                                                                                          9.9%; Score 309; DB 6; 22.3%; Pred. No. 4.6e-11;
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Pred. No. 4.6e-11;
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Pred. No. 4.6e-11;
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Pred. No. 4.6e-11;
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Pred. No. 4.6e-11;
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US2003032113-Al.
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                                                          9.9%;
                                                                                                                                                               9.9%;
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                                                          Query Match
Best Local Similarity
RESULT 1160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity RESULT 1165
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Best Local Similarity
RESULT 1166
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RESULT 1168
ID ABO02880 standard;
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RESULT 1169
                                                                                                                                                                          Best Local Similarity RESULT 1161
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RESULT 1162
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RESULT 1167
                                           06-FEB-2003.
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9.9%; Score 309; DB 6; Length 649; 22.3%; Pred. No. 4.6e-11;
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Pred. No. 4.6e-11;
                                                                                                                                                          Length 649;
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22.3%; Pred. No. 4.6e-11;
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                                                                                                                                                                                                                                                                                                                                                    ABU99929 standard; protein; 649 AA.
Novel human secreted and transmembrane protein PRO1865.
US2003013153-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABU98144 standard; protein; 649 AA.
Novel human secreted and transmembrane protein PRO1865.
US2003017544-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AB091850 standard; protein; 649 AA.
Novel human secreted and transmembrane protein PRO1865.
US20031027277-A1.
6-FEB-2003.
                                                                                  ABR94796 standard; protein; 649 AA.
Human secreted polypeptide PRO1865, SEQ ID NO:384
US2003044926-A1.
06-MAR-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABU86384 standard; protein; 649 AA.
Human secreted/transmembrane protein (PRO) #192
US2003036146-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABU67597 standard; protein; 649 AA.
Human secreted/transmembrane protein (PRO) #192
US2003036162-A1.
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Pred. No. 4.6e-11;
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Pred. No. 4.6e-11;
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Pred. No. 4.6e-11;
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Pred. No. 4.6e-11;
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Pred. No. 4.6e-11;
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Pred. No. 4.6e-11;
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Pred. No. 4.6e-11;
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Human PRO polypeptide #192.
US2003036140-Al.
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Human PRO polypeptide #192.
US2003036141-A1.
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Human PRO protein #192.
US2003036137-A1.
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Local Similarity 22.3%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                             Best Local Similarity
RESULT 1172
ID ABU98229 standard; pi
DE Novel human secreted
PN US2003013153-A1.
PD 16-JAN-2003.
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                                               Best Local Similarity RESULT 1170
                                                                                                                                                          Query Match
Best Local Similarity
RESULT 1171
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
RESULT 1173
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US2003040056-A1.
27-FEB-2003.
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Score 309; DB 6; Length 649;
Pred. No. 4.6e-11;
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                                                                        Length 649;
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9 9%; Score 309; DB 6; Length
Best Local Similarity 22.3%; Pred. No. 4.6e-11;

RESULT 1187

1D ABU72017 standard; protein; 649 AA.

Novel human secreted and transmembrane protein PRO1865.

PD 22-TRANSON.
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Novel human secreted and transmembrane protein PRO1865.
US2003018173-A1.
23-JAN-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABR92356 standard; protein; 649 AA.
Human secreted polypeptide PR01865, SEQ ID NO:384
US2003035160-A1.
20-FEB-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABR77418 standard; protein; 649 AA.
Human secreted polypeptide PRO1865, SEQ ID NO:384
US2003054474-A1.
                                                                                                                                                                                                                                                       ABR99543 standard; protein; 649 AA.
Human secreted polypeptide PRO1865, SEQ ID NO:384
US2003040063-A1.
27-FEB-2003.
                                                                                                                                                                                                                                                                                                                                                                          ABR98933 standard; protein; 649 AA.
Human secreted polypeptide PRO1865, SEQ ID NO:384
US2003040064-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABO16456 standard; protein; 649 AA.
Human secreted/transmembrane protein (PRO) #192.
US2003027267-A1.
06-FEB-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABO18997 standard; protein; 649 AA.
Human secreted/transmembrane protein (PRO) #192.
US2003044925-A1.
                                                                                                                                                                                                           Score 309; DB 6;
Pred. No. 4.6e-11;
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Pred. No. 4.6e-11;
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Pred. No. 4.6e-11;
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Pred. No. 4.6e-11;
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Pred. No. 4.6e-11;
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Pred. No. 4.6e-11;
                                                                     Score 309; DB 6;
Pred. No. 4.6e-11;
                                                                                                                                        Human secreted/transmembrane protein PRO1865.
US2003009013-A1.
                                                                                                                          ABO34000 standard; protein; 649 AA.
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(GETH ) GENENTECH INC.
                                                     (GETH ) GENENTECH INC.
Query Match
                                                                                                                                                                                             (GETH ) GENENTECH INC.
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RESULT 1181
                                                                                    Best Local Similarity
RESULT 1180
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Best Local Similarity
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Best Local Similarity
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Best Local Similarity
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Best Local Similarity
RESULT 1189
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Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                             09-JAN-2003
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Length 649;

Score 309; DB 6; Pred. No. 4.6e-11;

9.9%;

-2003.

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Query Match
Best Local Similarity
RESULT 1200
    US2003036148-A1
                                                                                                                                                                            Length 649;
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Pred. No. 4.6e-11;
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                                                                  Length 649;
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ABO00293 standard; protein; 649 AA.
Novel human secreted and transmembrane protein PRO1865.
US20030312101-A1.
                                                                                                                                                                                                                                                                                                                   RESULT 1192
ID ABU88844 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003036133-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABO06340 standard; protein; 649 AA.
Novel human secreted and transmembrane protein PRO1865.
US2003022294-A1.
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Novel human secreted and transmembrane protein PRO1865.
20-PEB-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABR59376 standard; protein; 649 AA.
Human secreted polypeptide PRO1865, SEQ ID NO:384
US2003027275-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABR66938 standard; protein; 649 AA.
Human secreted polypeptide PRO1865, SEQ ID NO:384.
                                                                                                        ABOI1625 standard; protein; 649 AA.
Human secreted/transmembrane protein (PRO) #192
US2003036124-A1.
                                                                                                                                                                                                                      ABO02270 standard; protein; 649 AA.
Human secreted/transmembrane protein (PRO) #192.
US2003040054-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                               ABU83539 standard; protein; 649 AA.
Human secreted/transmembrane protein (PRO) #192.
US2003036134-A1.
                                                                                                                                                                            Score 309; DB 6;
Pred. No. 4.6e-11;
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Pred. No. 4.6e-11;
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Pred. No. 4.6e-11;
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Pred. No. 4.6e-11;
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Human secreted/transmembrane protein (PRO) #192.
US203027324-A1.
06-FEB-2003.
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Human secreted/transmembrane protein (PRO) #192.
US2003036123-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 309; DB 6;
Pred. No. 4.6e-11;
                                                                Score 309; DB 6;
Pred. No. 4.6e-11;
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Best Local Similarity
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Best Local Similarity
RESULT 1196
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Best Local Similarity
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Best Local Similarity
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Best Local Similarity
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Best Local Similarity
RESULT 1190
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Best Local Similarity
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                                                13-FEB-2003.
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RESULT 1198
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RESULT 1199
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Query Match 9.9%; Score 309; DB 6; Length 649; Best Local Similarity 22.3%; Pred. No. 4.6e-11; RESULT 1202
                                                                              Length 649;
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Human secreted polypeptide PRO1865, SEQ ID NO:384.
US2003027266-A1.
06-FRB-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                      ABUĞ5760 standard; protein; 649 AA.
Human secreted/transmembrane protein, SEQ ID 384.
US2003036156-A1.
20-FRB-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 22.3%; Pred. No. 4.6e-11; RESULT 1205
ID ABO03795 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.PD 20-FEB-2003.
ABO16151 standard; protein; 649 AA.
Human secreted/transmembrane protein (PRO) #192.
US2003040060-A1.
27-FEB-2003.
                                                                                                                                ABO13857 standard; protein; 649 AA.
Human secreted/transmembrane protein (PRO) #192.
US2003044916-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABO15846 standard; protein; 649 AA.
Human secreted/transmembrane protein (PRO) #192.
US2003054483-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 309; DB 6;
Pred. No. 4.6e-11;
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Pred. No. 4.6e-11;
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Pred. No. 4.6e-11;
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Pred. No. 4.6e-11;
                                                                             9.9%; Score 309; DB 6; 22.3%; Pred. No. 4.6e-11;
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Pred. No. 4.6e-11;
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Pred. No. 4.6e-11;
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Best Local Similarity 22.3%; Pred. No. 4.6e-1.
DD ABUS6127 standard; protein; 649 AA.
DB Human secreted/transmembrane protein, PRO1865.
PN US2003022298-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 22.3%; Pred. RESULT 1204
ID ABOO7608 standard; protein; 649 AA. DE Human PRO polypeptide #192. PN US2003032117-A1.
                                                                                                                                                                                                                                                                  ABU71571 standard; protein; 649 AA. Human secreted polypeptide PRO1865. US2003013855-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABU72352 standard; protein; 649 AA.
Human PRO polypeptide #66.
US2002182638-A1.
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Best Local Similarity
RESULT 1203
                                                                           Query Match
Best Local Similarity
RESULT 1201
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RESULT 1206
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Best Local Similarity
RESULT 1207
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RESULT 1209
                                                                                                                                                                                               06-MAR-2003.
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Score 309; DB 6; Length 649; Pred. No. 4.6e-11;
                              Score 309; DB 6; Length 649; Pred. No. 4.6e-11;
                                                                                                                                                                                                                                                                 Length 649;
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Pred. No. 4.6e-11;
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Pred. No. 4.6e-11;
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                                                                                                                                                 Length 649;
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Pred. No. 4.6e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 649;
                                                                                                                                                                                          ABUSE400 standard; protein; 649 AA.
Novel human secreted and transmembrane protein PRO1865
US2003036117-A1.
20-FEB-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABR70154 standard; protein; 649 AA.
Human secreted polypeptide PRO1865, SEQ ID NO:384
US2003032138-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABR66987 standard; protein; 649 AA.
Human secreted polypeptide PRO1865, SEQ ID NO:384
US2003036132-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABR60227 standard; protein; 649 AA.
Human secreted polypeptide PRO1865, SEQ ID NO:384
US2003032137-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 309; DB 6;
Pred. No. 4.6e-11;
                                                                                                                                                Score 309; DB 6;
Pred. No. 4.6e-11;
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Pred. No. 4.6e-11;
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US2003017542-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                        ABO07913 standard; protein; 649 AA. Human PRO polypeptide #192. US2003032130-AI.
                                                                                                                                                                                                                                                                                                             ABU71303 standard; protein; 649 AA.
Human PRO1865 protein.
US2003036143-A1.
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ID ABO01628 standard; protein; 649 AA. BE Human PRO polypeptide #192. BD 09-JAN-2003. BD 09-JAN-2003. BD 09-JAN-2003. BA (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABU91025 standard; protein; 649 AA.
Human PRO polypeptide #66.
US2003018168-A1.
                                                                           ABU65455 standard; protein; 649 AA.
Human PRO polypeptide #192.
US2003032102-Al.
U3-FEB-2003.
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22.3%;
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                              9.9%;
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05-DEC-2002.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 1215
ID ABR69487 standard; p.
DE Human secreted polypt
PN US2003036132-A1.
                              Query Match
Bast Local Similarity
RESULT 1210
ID ABU65455 standard; p
DE Human PRO polypeptid
PN US2003032102-A1.
PD 13-FEB-2003.
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RESULT 1217
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Best Local Similarity
RESULT 1212
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Best Local Similarity
RESULT 1211
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Best Local Similarity
RESULT 1213
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Best Local Similarity
RESULT 1214
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Score 309; DB 6; Length 649;
Pred. No. 4.6e-11;
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Pred. No. 4.6e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 309; DB 6; Length 649; Pred. No. 4.6e-11;
                                                                                                                                                                         9.9%; Score 309; DB 6; Length 649; 22.3%; Pred. No. 4.6e-11;
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Novel human secreted and transmembrane protein PRO1865
US2003032123-A1.
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Novel human secreted and transmembrane protein PRO1865
                                                                                                                                                                                                                                                                                                                              Beet Local Similarity 22.3%; Pred. No. 4.6e-11; RESULT 1222
ID ABR68672 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865; SEQ ID NO:384.
PN US2003027274-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Beef Local Similarity 22.3%; Pred. No. 4.6e-11; RESULT 1223
DB Human secreted polypeptide PRO1865, SEQ ID No.384. PD 13-FEB-2003.
PD 13-FEB-2003.
PD 13-FEB-2003.
                                                                                                                                                                                            Best Local Similarity 22.3%; Pred. No. 4.6e-11; RESULT 1221
ID ABR65350 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003027268-A1.
                                                                                                                 SEQ ID NO:384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABU89154 standard; protein; 649 AA.
Human secreted/transmembrane protein (PRO) #192.
10.2003022297-A1.
30-AAN-2003.
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Human secreted/transmembrane protein (PRO) #192.
US2003032105-A1.
13-FEB-2003.
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Human secreted/transmembrane protein (PRO) #192.
US2003032111-A1.
13-FBB-2003.
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Pred. No. 4.6e-11;
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Pred. No. 4.6e-11;
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                                                                                             ABR67962 standard; protein; 649 AA.
Human secreted polypeptide PR01865,
US2003027269-A1.
06-FEB-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABU85464 standard; protein; 649 AA.
Human PRO polypeptide #192.
US2003022295-A1.
30-JAN-2003.
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                                   Query Match 9.9%;
Best Local Similarity 22.3%;
RESULT 1220
23-JAN-2003.
(GETH ) GENENTECH INC.
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RESULT 1224
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Best Local Similarity
RESULT 1226
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Best Local Similarity
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RESULT 1240
ID ABO08216
DE Human PI
PN US200304
     Length 649;
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Pred. No. 4.6e-11;
                                                                                                                                           Length 649;
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                                               ABU003800 standard, protein; 649 AA.
Novel human secreted and transmembrane protein PRO1865.
US2003032119-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABU86074 standard; protein; 649 AA.
Novel human secreted and transmembrane protein PRO1865.
US2003022300-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABU82361 standard; protein; 649 AA.
Novel human secreted and transmembrane protein PRO1865.
US2003036136-A1.
                                                                                                                                                                                           ABR65045 standard; protein; 649 AA.
Human secreted polypeptide PRO1865, SEQ ID NO:384.
US2003027253-A1.
06-FBB-2003.
                                                                                                                                                                                                                                                                                                                ABR68877 standard; protein; 649 AA.
Human secreted polypeptide PRO1865, SEQ ID NO:384.
US2003027271-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABR99238 standard; protein; 649 AA.
Human secreted polypeptide PRO1865, SEQ ID NO:384.
US2003040068-A1.
 9.9%; Score 309; DB 6; 22.3%; Pred. No. 4.6e-11;
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Human secreted/transmembrane protein (PRO) #192.
US2003036125-A1.
20-FEB-2003.
                                                                                                                                           Score 309; DB 6;
Pred. No. 4.6e-11;
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Pred. No. 4.6e-11;
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Pred. No. 4.6e-11;
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Pred. No. 4.6e-11;
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Pred. No. 4.6e-11;
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Human secreted/transmembrane protein (PRO) #192
US2003032109-A1.
13-FEB-2003.
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Human PRO polypeptide #192.
US2003027280-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABU87372 standard; protein; 649 AA.
Human PRO polypeptide #192.
US2003036138-AI.
                                                                                                                                         9.9%;
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                                                                                                                       (GETH ) GENENTECH INC.
                                                                                                                                         Query Match
Best Local Similarity
              Best Local Similarity RESULT 1230
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Best Local Similarity
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Best Local Similarity
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Best Local Similarity
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2382

2225

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Query Match 9.9%; Score 309; DB 6; Length 649; Beet Local Similarity 22.3%; Pred. No. 4.6e-11; RESULT 1245
                                                                              9.9%; Score 309; DB 6; Length 649; 22.3%; Pred. No. 4.6e-11;
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                                                                                                                                                                                                                                                                                        ABUG129 standard; protein; 649 AA.
Novel human secreted and transmembrane protein PRO1865.
US2003032104-A1.
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ID ABU94110 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003036155-A1.
PD 20-FEB-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                             ABUG6093 standard; protein; 649 AA.
Novel human secreted and transmembrane protein PRO1865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABU99963 standard; protein; 649 AA.
Novel human secreted and transmembrane protein PRO1865.
US2003022296-A1.
30-JAN-2003.
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ID ABR66633 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003027281-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABR59922 standard; protein; 649 AA.
Human secreted polypeptide PRO1865, SEQ ID NO:384
US2003032120-A1.
13-FEB-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABR91051 standard; protein; 649 AA.
Human secreted polypeptide PR01865, SEQ ID NO:384.
US2003040058-A1.
27-FRB-2003.
                                                                                                                                                                                                                                             Score 309; DB 6;
Pred. No. 4.6e-11;
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Pred. No. 4.6e-11;
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Pred. No. 4.6e-11;
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Pred. No. 4.6e-11
                                                                                                                                                           Human secreted/transmembrane protein PRO1865. US2003045684-A1.
ABO08218 standard; protein; 649 AA.
Human PRO polypeptide #192.
US2003040066-A1.
27-FEB-2003.
                                                                                                                                       ABU92541 standard; protein; 649 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABUBI211 standard, protein, 649 AA. Human secreted polypeptide PRO1865. US2003027212-A1.
                                                                                                                                                                                                                                                                                                                                                                                   9.9%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                          Query Match
Best Local Similarity
REGULT 1241
ID ABU92541 standard; p:
DE Human secreted/trans:
PD 06-WAR-2003.
PA (GETH ) GENENTECH IN
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Best Local Similarity
RESULT 1249
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Best Local Similarity
RESULT 1244
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20-FEB-2003.
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Best Local Similarity 22.3%; Score 309; DB 6; Length 649; RESULT 1251

ID ABUG4478 standard; protein; 649 AA.

BN US2003017540-A1.

Oner, March 2003.
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Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1252
ID ABLTJ360 standard; protein; 649 AA.

BE Human PRO polypeptide #192.

PNO US2003032106-A1.
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Pred. No. 4.6e-11;
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Pred. No. 4.6e-11;
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RESULT 1250

ID ABO53125 standard; protein; 649 AA.

BE Novel human secreted and transmembrane protein PRO1865.

PN US2003027986-A1.

PD 06-FEB-2003.

PA (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABU86994 standard; protein; 649 AA.
Novel human secreted and transmembrane protein PRO1865
US2003032131-A1.
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Human secreted polypeptide PRO1865, SEQ ID NO:384
US2003032139-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABR66023 standard; protein; 649 AA.
Human secreted polypeptide PRO1865, SEQ ID NO:384
US2003036165-A1.
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Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1254
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Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1253
ABM6669 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192
PN US2003032129-A1.
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Pred. No. 4.6e-11;
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Human PRO polypeptide #192.
US2003032103-A1.
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Human PRO polypeptide #192.
US2003022301-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AB004710 standard; protein; 649 AA.
Human PRO polypeptide #192.
US2003032107-A1.
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RESULT 1258
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Best Local Similarity 22.3%;
RESULT 1255
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(GETH ) GENENTECH INC.
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9.9%; Score 309; DB 6; Length 649; 22.3%; Pred. No. 4.6e-11;
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Pred. No. 4.6e-11;
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Novel human secreted and transmembrane protein PRO1865.
US2003036153-A1.
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RESULT 1269
ID ABU98328 standard; protein; 649 AA.

DE Novel human secreted and transmembrane protein PRO1865.
PN US2002183493-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABU31235 standard; protein; 649 AA.
Novel human secreted and transmembrane protein PRO1865
US2003036154-A1.
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9.9%; scott v. 6e-11;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1268
ID ABR71069 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003040069-A1.
ABR64740 standard; protein; 649 AA.
Human secreted polypeptide PRO1865, SEQ ID NO:384
US2003027262-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABO09743 standard; protein; 649 AA.
Human secreted/transmembrane protein (PRO) #192.
US2003044931-A1.
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Human secreted/transmembrane protein (PRO) #192.
US2003036150-A1.
                                                                                                                                                                                                                                                                                           ABU93056 standard; protein; 649 AA.
Human secreted/transmembrane protein (PRO) #192
US2003036142-A1.
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Pred. No. 4.6e-11;
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Best Local Similarity 22.3%; Pred.
RESULI 12.3%; Pred.
ID ABU87677 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
                                                                                                                                                                                                                                                                                                                                                                                                                                          ABU96015 standard; protein; 649 AA.
Human PRO polypeptide #192.
US2003036145-A1.
                                                                                                                                             ABU79665 standard; protein; 649 AA.
Human PRO polypeptide #192.
US2003032110-A1.
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                                                                              Query Match
Best Local Similarity
RESULT 1261
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Best Local Similarity
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Best Local Similarity
RESULT 1264
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Best Local Similarity
RESULT 1265
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Best Local Similarity
RESULT 1267
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Best Local Similarity
RESULT 1263
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06-FEB-2003
                             9.9%; Score 309; DB 6; Length 649; 22.3%; Pred. No. 4.6e-11;
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Pred. No. 4.6e-11;
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Pred. No. 4.6e-11;
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Pred. No. 4.6e-11;
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Pred. No. 4.6e-11;
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                                                                                                                                                              ABU89333 standard; protein; 649 AA.
Novel human secreted and transmembrane protein PRO1865.
US2003036634-A1.
20-PEB-2003.
(GETH ) GENENTECH INC.
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US2002183494-A1.
                                                                                                                                                                                                                                                                                                                                                                              ABR69849 standard; protein; 649 AA.
Human secreted polypeptide PRO1865, SEQ ID NO:384.
US2003032122-A1.
                                                                                                                                                                                                                                                                             ABU84759 standard; protein; 649 AA.
Human secreted/transmembrane protein (PRO) #192.
US2003032116-A1.
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                                                                                                                          9.9%; Score 309; DB 6; 22.3%; Pred. No. 4.6e-11;
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Pred. No. 4.6e-11;
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Pred. No. 4.6e-11;
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Human secreted/transmembrane protein (PRO) #192
US2003017543-A1.
                                                                 ABU91545 standard; protein; 649 AA, Human PRO polypeptide #192.
US2003032128-A1.
13-FEB-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABU80226 standard; protein; 649 AA.
Human PRO protein #192.
US2003036139-A1.
20-FEB-2003.
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Human PRO polypeptide #192.
US2003017541-A1.
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Human PRO polypeptide #66.
US2003027993-A1.
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(GETH ) GENENTECH INC.
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RESULT 1275
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Best Local Similarity
RESULT 1276
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Best Local Similarity
RESULT 1278
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Best Local Similarity
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RESULT 1274
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                                 Best Local Similarity
RESULT 1271
US2003022293-A1.
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PA (GETH ) GENENTECH INC.

Query Match

Query Match

Best Local Similarity 22.3%; Score 309; DB 6; Length 649;

Best Local Similarity 22.3%; Pred. No. 4.6e-11;

RESULT 1281

ID ABU10701 standard; protein; 649 AA.

DE Human secreted/transmembrane protein #192.

PN US2002127584-A1.

PD 12-SRP-2002.

PA (GETH ) GENENTECH INC.
                                                                                                                                                            vuery Match
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1282
                                                                                                                                                                                                                                                                                                                                Score 309; DB 6; Length 649;
Pred. No. 4.6e-11;
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Novel human secreted and transmembrane protein PRO1865.
US2003322140-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABO05115 standard; protein; 649 AA.
Novel human secreted and transmembrane protein PRO1865.
US2003008352-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABR70764 standard; protein; 649 AA.
Human secreted polypeptide PRO1865, SEQ ID NO:384.
US2003040076-A1.
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Human secreted polypeptide PRO1865, SEQ ID NO:384.
US2003035135-A1.
20-FEB-2003.
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US2003032118-A1.
13-PEB-2003.
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Human secreted/transmembrane protein (PRO) #192.
US2003044922-A1.
06-MAR-2003.
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Pred. No. 4.6e-11;
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Pred. No. 4.6e-11;
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Pred. No. 4.6e-11;
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Pred. No. 4.6e-11;
                                                                                                                                                                                                                                ABU72174 standard; protein; 649 AA. Human PRO polypeptide #66. US2003023042-A1. 30-JAN-2003. (GETH) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 22.3%; Pred. RESULT 1283
ID ABU95710 standard; protein; 649 AA. BN US2003032115-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABR95711 standard; protein; 649 AA.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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RESULT 1284
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Best Local Similarity
RESULT 1287
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Best Local Similarity
RESULT 1288
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Best Local Similarity
RESULT 1289
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Best Local Similarity
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us-09-943-780-69.ragspdi

Length 649;

Score 309; DB 6; Pred. No. 4.6e-11;

Length 649;

Score 309; DB 6; Pred. No. 4.6e-11;

Length 649;

Length 649;

Score 309; DB 6; Pred. No. 4.6e-11;

Length 649;

Score 309; DB 6; Pred. No. 4.6e-11;

Length 649;

Score 309; DB 6; Pred. No. 4.6e-11;

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9.9%; Score 309; DB 6; Length 649; 22.3%; Pred. No. 4.6e-11; 9.9%; Score 309; DB 6; Length 649; 22.3%; Pred. No. 4.6e-11; Best Local Similarity 22.3%; Pred. No. 4.6e-11; RESULT 1306
ID ABMI7355 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003054459-A1. ABR95101 standard; protein; 649 AA.
Human secreted polypeptide PRO1865, SEQ ID NO:384.
US2003044930-A1.
06-MAR-2003. ABR95406 standard; protein; 649 AA. Human secreted polypeptide PRO1865, SEQ ID NO:384. US2003040071-A1. RESULT 1303 ID ABM24917 standard; protein; 649 AA. DE Human secreted polypeptide PRO1865, SEQ ID NO:384 PN US2003104539-A1. RESULT 1305 ID ABR90441 standard; protein; 649 AA. DE Human secreted polypeptide PR01865, SEQ ID NO:384 PN US2003040075-A1. ADA78136 standard; protein; 649 AA. Human secreted/transmembrane protein (PRO) #192 US2003073180-A1. Query Match 9.9%; Score 309; DB 6; Best Local Similarity 22.3%; Pred. No. 4.6e-11; ABO03185 standard; protein; 649 AA. Human secreted/transmembrane protein (PRO) #192. US2003036131-A1. ABO35983 standard; protein; 649 AA. Human PRO polypeptide #192. US2003068701-A1. 10-APR-2003. (GETH ) GENENTECH INC. ABO44122 standard; protein; 649 AA. Human PRO polypeptide #192. US2003068755-A1. Best Local Similarity 22.3%; RESULT 1300 9.9%; 9.9%; 9.9%; 9.9%; 9.9%; 9.9%; 27-FEB-2003. (GETH ) GENENTECH INC. 20-MAR-2003. (GETH ) GENENTECH INC. 10-APR-2003. (GETH ) GENENTECH INC. 17-APR-2003. (GETH ) GENENTECH INC. (GETH ) GENENTECH INC. Best Local Similarity RESULT 1301 Query Match Best Local Similarity Local Similarity Query Match Best Local Similarity Local Similarity Local Similarity Query Match Best Local Similarity US2003068682-A1. 05-JUN-2003. 27-FEB-2003. 20-FEB-2003. 10-APR-2003 Query Match Query Match Query Match Query Match Query Match RESULT 1302 Best 9.9%; Score 309; DB 6; Length 649; 22.3%; Pred. No. 4.6e-11; Length 649; 9.9%; Score 309; DB 6; Length 649; 22.3%; Pred. No. 4.6e-11; Length 649; Length 649; Length 649; Length 649; 9.9%; Score 309; DB 6; Length 649; 22.3%; Pred. No. 4.6e-11; Length 649; Human secreted polypeptide PRO1865, SEQ ID NO:384. US2003054455-Al. 20-MAR-2003. ABRBIOO8 standard; protein; 649 AA. Human secreted polypeptide PRO1865, SEQ ID NO:384 US2003049741-A1. ABR81313 standard; protein; 649 AA. Human secreted polypeptide PR01865, SEQ ID NO:384 US2003049743-Al. Human secreted polypeptide PRO1865, SEQ ID NO:384. US2003068743-Al. Human secreted polypeptide PRO1865, SEQ ID NO:384 US2003054479-A1. ABM08078 standard; protein; 649 AA. Human secreted polypeptide PRO1865, SEQ ID NO:384. US2003068752-A1. Human secreted polypeptide PRO1865, SEQ ID NO:384 US20030469-Al. Query Match
Best Local Similarity 22.3%; Score 309; DB 6;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1293
ID ABM01009 standard; protein; 649 AA.
DE Human secreted polypeptide PR01865; SEQ ID NO:38
PN US2003049769-A1.
PP 13-MAR-2003.
PA (GETH ) GENENTECH INC. Jr 1296 ABO28916 standard; protein; 649 AA. Human secreted/transmembrane protein (PRO) #192 US2003068685-A1. ABO31661 standard; protein; 649 AA. Human secreted/transmembrane protein (PRO) #192 US2003068725-A1. ABO40558 standard; protein; 649 AA. Human secreted/transmembrane protein (PRO) #192. PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1296 Score 309; DB 6; Pred. No. 4.6e-11; 9.9%; Score 309; DB 6; 22.3%; Pred. No. 4.6e-11; 9.9%; Score 309; DB 6; 22.3%; Pred. No. 4.6e-11; Score 309; DB 6; Pred. No. 4.6e-11; ABM77432 standard; protein; 649 AA. 9.9%; 9.9%; PA (GETH ) GENENTECH INC. QUERY MATCh BEST LOCAL SIMILATILY 22.3%; RESULT 1298 10-APR-2003. (GETH ) GENENTECH INC. 13-MAR-2003. (GETH ) GENENTECH INC. 13-MAR-2003. (GETH ) GENENTECH INC. 10-APR-2003. (GETH ) GENENTECH INC. GENENTECH INC. (GETH ) GENENTECH INC Best Local Similarity
RESULT 1295
ID ABM77432 standard; pi
DE Human secreted polype
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC Query Match Best Local Similarity RESULT 1294 Best Local Similarity RESULT 1297 Best Local Similarity RESULT 1291 Best Local Similarity RESULT 1292 Local Similarity 10-APR-2003 10-APR-2003 Query Match Query Match Query Match Query Match

Score 309; DB 6; Length 649; Pred. No. 4.6e-11;

Score 309; DB 6; Length 649; Pred. No. 4.6e-11;

Human secreted polypeptide PRO1865, SEQ ID NO:384

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9.9%; Score 309; DB 6; Length 649; 22.3%; Pred. No. 4.6e-11;
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Pred. No. 4.6e-11;
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Pred. No. 4.6e-11;
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Pred. No. 4.6e-11;
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Pred. No. 4.6e-11;
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Human secreted polypeptide PRO1865, SEQ ID NO:384.
US2003064452-A1.
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Human secreted polypeptide PRO1865, SEQ ID NO:384.
102203068704.A1.
10-APR-2003.
(GETH ) GENENTECH INC.
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Human secreted polypeptide PRO1865, SEQ ID NO:384.
US2003073183-A1.
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Human secreted polypeptide PRO1865, SEQ ID NO:384
US2003068705-A1.
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Human secreted polypeptide PRO1865, SEQ ID NO:384
US2003054473-Al.
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Human secreted polypeptide PRO1865, SEQ ID NO:384
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Human secreted polypeptide PRO1865, SEQ ID NO:384
US2003068722-A1.
RESULT 1309

ID ADB17189 standard; protein; 649 AA.

DE Human transmembrane PRO polypeptide (SeqID 132).

PN US2003050462-A1.

PD 13-MAR-2003.

PA (GETH ) GENENTECH INC.
                                                                                                    Score 309; DB 6;
Pred. No. 4.6e-11;
                                                                                                                                                  ABO21644 standard; protein; 649 AA.
Human secreted/transmembrane protein (PRO) #192
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Pred. No. 4.6e-11;
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RESULT 1313
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RESULT 1316
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Best Local Similarity 22.3%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Query Match
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(GETH ) GENENTECH INC.
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RESULT 1315
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Best Local Similarity
                                                                                                              Best Local Similarity RESULT 1310
                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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20-MAR-2003.
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cuery Match 9.9%; Score 309; DB 6; Length 649; Best Local Similarity 22.3%; Pred. No. 4.6e-11; RESULT 1322 ID ABM11738 standard; protein; 649 AA. DE Human secreted polypeptide PRO1865, SEQ ID NO:384. PM US2003064447-A1.
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                                                          Length 649;
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Human secreted polypeptide PRO1865, SEQ ID NO:384.
US2003064462-A1.
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Human secreted polypeptide PRO1865, SEQ ID NO:384.
US2003073184-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABM16135 standard; protein; 649 AA.
Human secreted polypeptide PRO1865, SEQ ID NO:384.
US2003064463-A1.
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Human secreted polypeptide PR01865, SEQ ID NO:384.
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ID ABM29187 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384
PN US2003069121-A1.
                                                                                                                                                                                                                                                                                                                                                                                                               ABO24727 standard; protein; 649 AA.

Human secreted/transmembrane protein (PRO) #192.
                                                                                                              ABO48224 standard; protein; 649 AA.
Human secreted/transmembrane protein (PRO) #192
US2003049749-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABO27696 standard; protein; 649 AA.
Human secreted/transmembrane protein (PRO) #192.
US2003064451-A1.
                                                                                                                                                                                                                    Score 309; DB 6;
Pred. No. 4.6e-11;
                                                          Score 309; DB 6;
Pred. No. 4.6e-11;
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Pred. No. 4.6e-11;
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Pred. No. 4.6e-11;
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Best Local Similarity 22.3%; Pred. No. 4.6e-11;
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                                                      9.9%;
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RESULT 1321
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Best Local Similarity 22.3%;
RESULT 1320
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Best Local Similarity 22.3%;
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(GETH ) GENENTECH INC.
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GETH ) GENENTECH INC.
Query Match
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
US2003104549-A1.
05-JUN-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 1324
                                                                    Best Local Similarity
RESULT 1319
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RESULT 1323
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Length 649;

Score 309; DB 6; Pred. No. 4.6e-11;

Length 649;

Score 309; DB 6; Pred. No. 4.6e-11;

Length 649;

Score 309; DB 6; Pred. No. 4.6e-11;

Match

Query

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9.9%; Score 309; DB 6; Length 649; 22.3%; Pred. No. 4.6e-11;
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Human secreted polypeptide PRO1865, SEQ ID NO:384.
US2003044929-A1.
06-MAR-2003.
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Ukunan secreted polypeptide PRO1865, SEQ ID NO:384.
US2003064465-A1.
03-APR-2003.
                                                                                                                                                                                                                                                                                                                  Human secreted/transmembrane polypeptide PRO 1865.
US2003018172-A1.
23-JAN-2003.
(GETH ) GENENTECH INC.
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Human secreted polypeptide PRO1865, SEQ ID NO:384
US2003044917-A1.
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Human secreted polypeptide PRO1865, SEQ ID NO:384
US2003059880-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABO17066 standard; protein; 649 AA.
Human secreted/transmembrane protein (PRO) #192.
US2003054470-A1.
                                                                                                                                                                  ABO02575 standard; protein; 649 AA.
Human secreted/transmembrane protein (PRO) #192.
US2003040061-A1.
27-FEB-2003.
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                                    AB003490 standard; protein; 649 AA.
Human secreted/transmembrane protein (PRO) #192
   22.3%; Pred. No. 4.6e-11;
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Best Local Similarity 22.3%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 1339
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RESULT 1340
Best Local Similarity RESULT 1337
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RESULT 1338
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                                                                         US2003036127-A1.
20-FEB-2003.
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RESULT 1341
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Pred. No. 4.6e-11;
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ID ABM76213 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PD US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) CENTRAL
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Human secreted polypeptide PRO1865, SEQ ID NO:384.
US2003104543-A1.
                                                                                                            ABM21257 standard; protein; 649 AA.
Human secreted polypeptide PRO1865, SEQ ID NO:384.
US2003068707-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABM76517 standard; protein; 649 AA.
Human secreted polypeptide PRO1865, SEQ ID NO:384.
US2003082717-A1.
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Human secreted polypeptide PRO1865, SEQ ID NO:384.
US2003104542-A1.
05-JUN-2003.
                                                                                                                                                                                                                                                     ABM05603 standard; protein; 649 AA.
Human secreted polypeptide PRO1865, SEQ ID NO:384
US2003073175-A1.
                                                                                                                                                                                                                                                                                                                                                                                                           ABC41473 standard; protein; 649 AA.
Human secreted/transmembrane protein (PRO) #192.
US2003068695-A1.
10-ABR-2003.
(GETH ) GENENTECH INC.
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Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1329
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Pred. No. 4.6e-11;
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Pred. No. 4.6e-11;
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Pred. No. 4.6e-11;
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ABO36288 standard; protein; 649 AA.
Human PRO polypeptide #192.
US2003068703-A1.
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 1332
ID ABOA3817 standard; pr
DE Human PRO polypeptide
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC
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Best Local Similarity
RESULT 1333
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Best Local Similarity
RESULT 1330
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Best Local Similarity
RESULT 1335
                                                                       Best Local Similarity RESULT 1328
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   US2003068699-A1.
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                       10-APR-2003
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Best Local S
RESULT 1336
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RESULT

Score 309; DB 6; Length 649; Pred. No. 4.6e-11;

Length 649;

Score 309; DB 6; Pred. No. 4.6e-11;

Length 649;

Length 649;

Length 649;

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vuery Match 9.9%; Score 309; DB 6; Length 649; Best Local Similarity 22.3%; Pred. No. 4.6e-11; RESULT 1360
   9.9%; Score 309; DB 6; Length 649; 22.3%; Pred. No. 4.6e-11;
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Novel human secreted and transmembrane protein PRO1865.
US2003069394-A1.
                                                                                                                                                                                                         ABMI0518 standard; protein; 649 AA.
Human secreted polypeptide PRO1865, SEQ ID NO:384.
US2003069407-A1.
                                                                                                                                                                                                                                                                                                                                                         ABMI2043 standard; protein; 649 AA.
Human secreted polypeptide PRO1865, SEQ ID NO:384
US2003104555-A1.
(GETH ) GENENTECH INC.
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Human secreted polypeptide PRO1865, SEQ ID NO:384
US2003054481-A1.
                                                                                                                                                                                                                                                                                         Query Match
Beet Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1358
                                                                            Human secreted/transmembrane protein (PRO) #192 US2003068776-A1.
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Human secreted/transmembrane protein (PRO) #192
US2003032134-A1.
13-FEB-2003.
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Human transmembrane PRO polypeptide (SegID 132)
US2003050465-A1.
                                                                                                                                                   9.9%; Score 309; DB 6; 22.3%; Pred. No. 4.6e-11;
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Pred. No. 4.6e-11;
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Pred. No. 4.6e-11;
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Pred. No. 4.6e-11
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13-Mab-200
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US2003049768-A1.
                                                         ABO39643 standard; protein; 649 AA
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Best Local Similarity 22.3%;
RESULT 1361
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
               Best Local Similarity
RESULT 1356
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Best Local Similarity
RESULT 1363
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ID ABO52189 standard;
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     Query Match
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                   Length 649;
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Pred. No. 4.6e-11;
                                                         (GETH ) GENENTECH INC.

Query Match
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1348
ID ABR88001 standard; protein; 649 AA.
PD Human secreted polypeptide Protein PD PD IO-APR-2007
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9.9%; Score 309; DB 6; L.

Best Local Similarity 22.3%; Pred. No. 4.6e-11;

RESULT 1352

ID ABM05033 standard; protein; 649 AA.

DE Human secreted polypeptide PR01865, SEQ ID NO:384.

PN US22003068727-A1.
                                                                                                                                                                                                                        ABR88001 standard; protein; 649 AA.
Human secreted polypeptide PRO1865, SEQ ID NO:384
US2003068718-A1.
                                                                     ABR93576 standard; protein; 649 AA.
Human secreted polypeptide PRO1865, SEQ ID NO:384
US2003054478-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABM00993 standard; protein; 649 AA.
Human secreted polypeptide PRO1865, SEQ ID NO:384
US2003068772-Al.
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Human secreted/transmembrane protein (PRO) #192.
US2003064454-A1.
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Human secreted/transmembrane protein (PRO) #192
US2003064461-A1.
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Human secreted/transmembrane protein (PRO) #192.
US2003068714-A1.
                   Score 309; DB 6;
Pred. No. 4.6e-11;
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Pred. No. 4.6e-11;
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Pred. No. 4.6e-11;
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Pred. No. 4.6e-11;
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Human PRO polypeptide #192.
US2003068724-Al.
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Human PRO polypeptide #192.
US2003068758-A1.
                 9.9%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Query Match
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 1347
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RESULT 1349
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RESULT 1350
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RESULT 1355
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Length 649;

Length 649

Length 649;

RESULT 1354

Length 649; Score 309; DB 6; Length 649; Pred. No. 4.6e-11; Length 649; ABM18575 standard; protein; 649 AA. Human secreted polypeptide PRO1865, SEQ ID NO:384. US2003054480-A1. Auman secreted polypeptide PRO1865, SEQ ID NO:384. RESULT 1375
ID ABM35510 standard; protein; 649 AA.
DB Human secreted polypeptide PRO1865, SEQ ID NO:384
PN US2003073179-A1. RESULT 1376 ID ABM31273 standard; protein; 649 AA. DE Human secreted polypeptide PRO1865, SEQ ID NO:384 PN US2003087374-A1. ABO40863 standard; protein; 649 AA. Human secreted/transmembrane protein (PRO) #192. US2003068684-A1. Score 309; DB 6; Pred. No. 4.6e-11; Score 309; DB 6; Pred. No. 4.6e-11; Score 309; DB 6; Pred. No. 4.6e-11; ABO50359 standard; protein; 649 AA. Human secreted/transmembrane protein (PRO) #192 US2003049777-A1. Score 309; DB 6; Pred. No. 4.6e-11; Human secreted/transmembrane protein (PRO) #192 US2003040055-A1. Human secreted/transmembrane protein (PRO) #192 US2003036164-A1. ABO06035 standard; protein; 649 AA. Human secreted/transmembrane protein (PRO) #192 US2003040074-A1. 27-FEB-2003. Score 309; DB 6; Pred. No. 4.6e-11; Query Match 9.9%; Score Best Local Similarity 22.3%; Pred. RESULT 1377
ID ABO52799 standard; protein; 649 AA. DE Human PRO polypeptide #192. Query Match
Best Local Similarity 22.3%; Pred.
RESULT 1379
ID ABU99353 standard; protein; 649 AA. ABO04405 standard; protein; 649 AA 9.9%; 9.9%; 9.9%; 9.9%; 9.9%; Query Match 9.9%; Best Local Similarity 22.3%; RESULT 1378 Query Match Best Local Similarity 22.3%; 20-MAR-2003. (GETH ) GENENTECH INC. 17-APR-2003. (GETH ) GENENTECH INC. 13-MAR-2003. (GETH ) GENENTECH INC. 13-MAR-2003. (GETH ) GENENTECH INC. 27-MAR-2003. (GETH ) GENENTECH INC. (GETH ) GENENTECH INC. Best Local Similarity RESULT 1382 Query Match Best Local Similarity Best Local Similarity Query Match Best Local Similarity Query Match Best Local Similarity RESULT 1381 08-MAY-2003. 27-FEB-2003. 20-FEB-2003. 10-APR-2003 Query Match Query Match RESULT 1383

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9.9%; Score 309; DB 6; Length 649; 22.3%; Pred. No. 4.6e-11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 309; DB 6; Length 649;
Pred. No. 4.6e-11;
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                                                                                                                                                                  Length 649;
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Human secreted polypeptide PRO1865, SEQ ID NO:384.
US2003067478-A1.
                                                             ABR80703 standard; protein; 649 AA.
Human secreted polypeptide PRO1865, SEQ ID NO:384,
US2003049740-A1.
                                                                                                                                                                                                                       ABM01314 standard; protein; 649 AA.
Human secreted polypeptide PRO1865, SEQ ID NO:384
US2003049770-Al.
                                                                                                                                                                                                                                                                                                                                                         RESULT 1386
ID ABR88916 standard, protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384
PN US2003073169-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABM13568 standard; protein; 649 AA.
Human secreted polypeptide PRO1865, SEQ ID NO:384
US2003064457-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABM20952 standard; protein; 649 AA.
Human secreted polypeptide PRO1865, SEQ ID NO:384.
US2003068711-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABC42083 standard; protein; 649 AA.
Human secreted/transmembrane protein (PRO) #192.
US200309745-A1.
13-MAR-2003.
(GETH ) GENENTECH INC.
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Human secreted/transmembrane protein (PRO) #192.
US2003049751-A1.
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Human secreted/transmembrane protein (PRO) #192.
US2003068773-A1.
                                                                                                                                                              9.9%; Score 309; DB 6; 22.3%; Pred. No. 4.6e-11;
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Pred. No. 4.6e-11;
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Best Local Similarity 22.3%;
RESULT 1391
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Best Local Similarity 22.3%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
Query Match
                                                                                                                       13-MAR-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Query Match
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RESULT 1384
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RESULT 1390
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Length 649;
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ABM32968 standard; protein; 649 AA.
Human secreted polypeptide PRO1865, SEQ ID NO:384.
US2003073185-A1.
                                                                                                                                                                    ABM22782 standard; protein; 649 AA.
Human secreted polypeptide PRO1865, SEQ ID NO:384.
US2003087373-A1.
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Human secreted polypeptide PRO1865, SEQ ID NO:384.
US2003049772-A1.
                                                                                                                                                                                                                                                                                                                     ABW74993 standard; protein; 649 AA.
Human secreted polypeptide PRO1865, SEQ ID NO:384.
US2003096353-A1.
22-MAY-2003.
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Human secreted polypeptide PRO1865, SEQ ID NO:384
US2003054458-A1.
20-MAR-2003.
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Human secreted polypeptide PRO1865, SEQ ID NO:384.
US2003059886-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABR86476 standard; protein; 649 AA.
Human secreted polypeptide PRO1865, SEQ ID NO:384.
US2003049758-A1.
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Human secreted polypeptide PRO1865, SEQ ID NO:384.
US2003064448-A1.
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Human secreted polypeptide PRO1865, SEQ ID NO:384.
US2003064456-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADA79928 standard; protein; 649 AA.
Human secreted/transmembrane protein (PRO) #192.
US2003073173-A1.
                                                                                                        9.9%; Score 309; DB 6; 22.3%; Pred. No. 4.6e-11;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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                                                                                                                     Best Local Similarity
RESULT 1394
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RESULT 1396
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20-MAR-2003. (GETH ) GENENTECH INC. 20-MAR-2003. (GETH ) GENENTECH INC. INC. (GETH ) GENENTECH INC. GENENTECH INC. Local Similarity Best Local Similarity RESULT 1419 Local Similarity Local Similarity Query Match Best Local Similarity RESULT 1415 Query Match Best Local Similarity RESULT 1416 22-MAY-2003. (GETH ) GENENTECH 13-FEB-2003. 20-MAR-2003. 13-MAR-2003 13-MAR-2003 Query Match Query Match Query Match Query Match (GETH) RESULT 1418 RESULT 1420 Best BERGE Length 649; 9.9%; Score 309; DB 6; Length 649; 22.3%; Pred. No. 4.6e-11; 9.9%; Score 309; DB 6; Length 649; 22.3%; Pred. No. 4.6e-11; Length 649; ABM23392 standard; protein; 649 AA. Human secreted polypeptide PRO1865, SEQ ID NO:384. US2003068753-A1. Human secreted polypeptide PRO1865, SEQ ID NO:384. ABM24002 standard; protein; 649 AA. Human secreted polypeptide PRO1865, SEQ ID NO:384 US2030368735-Al. 10-APR-2003. ABM22172 standard; protein; 649 AA. Human secreted polypeptide PRO1865, SEQ ID NO:384. US2003068742-A1. ABM28577 standard; protein; 649 AA. Human secreted polypeptide PRO1865, SEQ ID NO:384. 022003082715-A1. 01-MAY-2003. ABM28882 standard; protein; 649 AA.
Human secreted polypeptide PRO1865, SEQ ID NO:384.
US2003082716-A1.
01-MAY-2003. ABM66526 standard; protein; 649 AA. Human secreted polypeptide PRO1865, SEQ ID NO:384. US2003068737-A1. RESULT 1407

ID ABOJ7813 standard; protein; 649 AA.

BE Human secreted/transmembrane protein (PRO) #192.

PD 10-APR-2003.

PD 10-APR-2003.

PD 10-APR-2003. RESULT 1403 ID ABO2921 standard; protein; 649 AA. DE Human secreted/transmembrane protein (PRO) #192 PN US2003068693-A1. Score 309; DB 6; Pred. No. 4.6e-11; Query Match 9.9%; Score 309; DB 6; Best Local Similarity 22.3%; Pred. No. 4.6e-11; RESULT 1404 Score 309; DB 6; Pred. No. 4.6e-11; 9.9%; Score 309; DB 6; 22.3%; Pred. No. 4.6e-11; Score 309; DB 6; Pred. No. 4.6e-11; 9.9%; 9.9%; 9.9%; 9.9%; Query Match 9.9%; Best Local Similarity 22.3%; RESULT 1406 9.9%; 10-APR-2003. (GETH ) GENENTECH INC. 10-APR-2003. (GETH ) GENENTECH INC. 10-APR-2003. (GETH ) GENENTECH INC. 05-JUN-2003. (GETH ) GENENTECH INC. (GETH ) GENENTECH INC. 10-APR-2003. (GETH ) GENENTECH INC. (GETH ) GENENTECH INC. Best Local Similarity RESULT 1410 Best Local Similarity RESULT 1408 Query Match Best Local Similarity Local Similarity Query Match Best Local Similarity Best Local Similarity RESULT 1409 Best Local Similarity RESULT 1411 Query Match Query Match Query Match Query Match Query Match Query Match

RESULT 1405

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Score 309; DB 6; Length 649; Pred. No. 4.6e-11;
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Novel human secreted and transmembrane protein PRO1865.
US2003055222-A1.
20-MAR-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                     Human secreted polypeptide PRO1865, SEQ ID NO:384. US2003100061-A1. 29-MAY-2003. (GETH ) GENENTECH INC.
RESULT 1412
ID ABM34188 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003095359-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABR85866 standard; protein; 649 AA.
Human secreted polypeptide PRO1865, SEQ ID NO:384.
US2003049753-A1.
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Human secreted polypeptide PRO1865, SEQ ID NO:384
US2003054460-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABR99848 standard; protein; 649 AA.
Human secreted polypeptide PRO1865, SEQ ID NO:384
US2003049763-A1.
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Human secreted polypeptide PR01865, SEQ ID NO:384
                                                                                                                                                                                                                                                                                                                                              ABO20424 standard; protein; 649 AA.
Human secreted/transmembrane protein (PRO) #192.
US2003032125-A1.
                                                                                                                         Score 309; DB 6;
Pred. No. 4.6e-11;
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Human secreted/transmembrane protein (PRO) #192
US2003054477-A1.
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Pred. No. 4.6e-11;
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Pred. No. 4.6e-11;
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Pred. No. 4.6e-11;
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                                                                                                                   Best Local Similarity 22.3%;
RESULT 1413
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RESULT 1417
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Best Local Similarity 22.3%; Pred. No. 4.6e-11; RESULT 1431
                                        Length 649;
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Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1428
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Human secreted polypeptide PRO1865, SEQ ID NO:384.
US2003068736-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABM29492 standard; protein; 649 AA.
Human secreted polypeptide PRO1865, SEQ ID NO:384.
US2003068679-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABM20647 standard; protein; 649 AA.
Human secreted polypeptide PR01865, SEQ ID NO:384.
US2003104557-A1.
05-JUN-2003.
                                                                                       ABM00704 standard; protein; 649 AA.
Human secreted polypeptide PRO1865, SEQ ID NO:384
US2003073172-A1.
17-APR-2003.
                                      9.9%; Score 309; DB 6; 22.3%; Pred. No. 4.6e-11;
                                                                                                                                                                  9.9%; Score 309; DB 6; 22.3%; Pred. No. 4.6e-11;
                                                                                                                                                                                                                   ABO29831 standard; protein; 649 AA.
Human secreted/transmembrane protein (PRO) #192
US2003068700-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AB038423 standard; protein; 649 AA.
Human secreted/transmembrane protein (PRO) #192.
US2003068767-A1.
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Best Local Similarity 22.3%; Pred. No. 4.6e-11;
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Pred. No. 4.6e-11;
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Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1427
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Human secreted/transmembrane protein (PRO) #192
US2003092121-A1.
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Human secreted/transmembrane protein (PRO) #192.
US2003027276-A1.
06-FEB-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AB045723 standard; protein; 649 AA. Human PRO polypeptide #192. US2003073182-A1.
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Best Local Similarity 22.3%;
RESULT 1426
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PA (GETH ) GENENTECH INC.
QUERY MAICH
9
BEST Local Similarity 22.
RESULT 1430
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Best Local Similarity 2
RESULT 1423

ID ABO29831 stander

DE Human secret

PN US20036

PA
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
RESULT 1429
                                                       Best Local Similarity
 US2003073172-A1.
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Best Local Similarity 22.3%; Score 309; DB 6; Length 649; RESULT 1434
DB Human percent; FAO No. 4.6e-11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 649;
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Human secreted polypeptide PRO1865, SEQ ID NO:384, US200306446-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABR81618 standard; protein; 649 AA.
Human secreted polypeptide PRO1865, SEQ ID NO:384
US2003049744-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABM78042 standard; protein; 649 AA.
Human secreted polypeptide PRO1865, SEQ ID NO:384.
US2003049783-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABM13873 standard; protein; 649 AA.
Human secreted polypeptide PRO1865, SEQ ID NO:384.
US2003064458-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABR89831 standard; protein; 649 AA.
Human secreted polypeptide PRO1865, SEQ ID NO:384.
US200307171-A1.
17-APR-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABM26747 standard; protein; 649 AA.
Human secreted polypeptide PRO1865, SEQ ID NO:384.
US2003032121-A1.
13-FEB-2003.
ABO18387 standard; protein; 649 AA.
Human secreted/transmembrane protein (PRO) #192
US203044920-A1.
06-WAR-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 9.9%; Score 309; DB 6; Best Local Similarity 22.3%; Pred. No. 4.6e-11; RESULT 1440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABO28611 standard; protein; 649 AA.
Human secreted/transmembrane protein (PRO) #192.
US2003064460-A1.
                                                                                                                                                                                                                        Score 309; DB 6;
Pred. No. 4.6e-11;
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Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1435
                                                                                    Score 309; DB 6;
Pred. No. 4.6e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 9.9%; Score 309; DB 6; Best Local Similarity 22.3%; Pred. No. 4.6e-11;
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                                                                                                                                                                                                                                                                               ABO23119 standard; protein; 649 AA.
Human PRO polypeptide #192.
US2003054461-A1.
20-MAR-2003.
(GETH ) GENENTECH INC.
                                                                                                Best Local Similarity 22.3%; Pred. RESULT 1432
ID ABO22814 standard; protein; 649 AA. BN US2003027265-A1.
                                                                                  9.9%;
                                                                                                                                                                                                                           9.9%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 1439
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Best Local Similarity
RESULT 1438
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RESULT 1433
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us-09-943-780-69.ragspdi

Query Match

Best Local RESULT 1442

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9.9%; Score 309; DB 6; Length 649; 22.3%; Pred. No. 4.6e-11;
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Human secreted polypeptide PRO1865, SEQ ID NO:384
US2003040059-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABR96993 standard; protein; 649 AA.
Human secreted polypeptide PRO1865, SEQ ID NO:384
US2003054462-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABM17050 standard; protein; 649 AA.
Human secreted polypeptide PRO1865, SEQ ID NO:384
US2003040078-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 22.3%; Pred. No. 4.6e-11; RESULT 1457

ID ABO21034 standard; protein; 649 AA.

DE Human secreted/transmembrane protein (PRO) #192.

PN US2003032132-A1.
                                                                      Human secreted/transmembrane protein (PRO) #192
US2003049750-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                         9.9%; Score 309; DB 6; 22.3%; Pred. No. 4.6e-11;
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Human secreted/transmembrane protein (PRO) #192.
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Pred. No. 4.6e-11;
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Human secreted/transmembrane protein (PRO) #192.
US2003044918-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.9%; Score 309; DB 6; 22.3%; Pred. No. 4.6e-11;
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Pred, No. 4.6e-11;
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Pred. No. 4.6e-11;
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Pred. No. 4.6e-11;
                                                                                                                                                                                       Human PRO polypeptide #192.
US2003049766-A1.
                                                                                                                                                                                                                                                                                                                                     Human PRO polypeptide #192.
US2003049767-Al.
                                                        protein; 649 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABM12348 standard; protein; 649 AA
                                                                                                                                                                                                                                                                                           9.9%;
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Best Local Similarity 22.3%;
                                                                                                                                             Query Match 9.9%;
Best Local Similarity 22.3%;
RESULT 1451
                                                                                                         13-MAR-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Query Match
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               Best Local Similarity RESULT 1450
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Best Local Similarity
RESULT 1453
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Best Local Similarity
RESULT 1455
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Best Local Similarity
                                                        ABO48529 standard;
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Best Local Similarity
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                                     Score 309; DB 6; Length 649;
Pred. No. 4.6e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 649;
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Pred. No. 4.6e-11;
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                                                                                                                                                                                 Length 649;
                                                                                                                                                                                                                                   ABMO7468 standard; protein; 649 AA.

Human secreted polypeptide PRO1865, SEQ ID NO:384.

N US2003068702-A1.

D IO-APR-2003.

A (GETH ) GENENTECH INC.

Query Match

Best Local Similarity 22.3%; Pred. No. 4.6e-11;
                                                                                                                                                                                                                                                                                                                                                                                  ABM04059 standard; protein; 649 AA.
Human secreted polypeptide PRO1865, SEQ ID NO:384.
US2003068734-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABM25222 standard; protein; 649 AA.
Human secreted polypeptide PRO1865, SEQ ID NO:384,
US2003104540-Al.
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Human secreted/transmembrane protein (PRO) #192.
US2003049747-A1.
PD 03-APR-2003.

Query (GETH ) GENENTECH INC.

Query Match
Beet Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1441

ID ABO30441 standard; protein; 649 AA.

DE Human secreted/transmembrane protein (PRO) #192.
PN US2003064464-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Beet Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABO47614 standard; protein; 649 AA.
Human secreted/transmembrane protein (PRO) #192.
US2003049742-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABO37203 standard; protein; 649 AA.
Human secreted/transmembrane protein (PRO) #192
US2003068719-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABO41778 standard; protein; 649 AA.
Human secreted/transmembrane protein (PRO) #192
US2003068729-A1.
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Pred. No. 4.6e-11;
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Pred. No. 4.6e-11;
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Pred. No. 4.6e-11;
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Pred. No. 4.6e-11;
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Pred. No. 4.6e-11;
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US2003068738-Al.
                                                                                                                                                                                 9.9%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
RESULT 1448
ID ABO47614 standard; pi
DE Human secreted/transn
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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Best Local Similarity
RESULT 1447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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Best Local Si
RESULT 1449
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Query Match

Best Local RESULT 1446

Query Match Best Local S

Score 309; DB 6; Length 649; Pred. No. 4.6e-11;

Length 649;

Score 309; DB 6; Pred. No. 4.6e-11;

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Best Local Similarity 22.3%; Score 309; DB 6; Length 649; RESULT 1469

ID ABM20037 standard; protein: 640 **
                                                                Thuman secreted polypeptide PRO1865, SEQ ID NO:384.

TO 05-JUN-2003.

A (GETH ) GENENTECH INC.

PARTH PARTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 22.3%; Score 309; DB 6; L RESULT 1473

ID ARRYL679 standard; protein; 649 AA.

DE Human secreted polypeptide PRO1865, SEQ ID NO:384.

PN US2003032133-A1.

Ouerv March
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 22.3%; Score 309; DB 6; L RESULT 1475

ID ARR98628 standard; protein; 649 AA.

DE Human secreted polypeptide PRO1865, SEQ ID NO:384.

PD US2003036129-A1.

Oner, Mar.
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Human secreted polypeptide PRO1865, SEQ ID NO:384.
US2003032135-A1.
13-FRB-2003.
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Human secreted polypeptide PRO1865, SEQ ID NO:384
US2003054467-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABR84951 standard; protein; 649 AA.
Human secreted polypeptide PRO1865, SEQ ID NO:384
US2003040057-A1.
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Human secreted/transmembrane protein (PRO) #192.
US2003049752-A1.
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ID ABO06998 standard; protein; 649 AA.

DR Human secreted/transmembrane protein (PRO) #192.

PD VS2003040053-A1.
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Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1474
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Beet Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1478
                                                                                                                                                                                                                                                       AB046943 standard; protein; 649 AA.
Human PRO polypeptide #192.
US2003049762-Al.
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Human PRO polypeptide #192.
US2003049765-A1.
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Best Local Similarity 22.3%;
RESULT 1471
                                                                                                                                                                                                                                                                                                                   13-MAR-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 1477
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DE Human secreted polypeptide PRO1865, SEQ ID NO:384.

PN US2003066441-Al.

PD 03-APR-2003.

Query Match
Best Local Similarity 22.3%; Pred. No. 4.6e-11;

RESULT 1462

ID ABM14788 standard; protein; 649 AA.

DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
                         Human secreted polypeptide PRO1865, SEQ ID NO:384.
US2003064445-A1.
                                                                                                                                                                  ABMIG440 standard; protein; 649 AA.
Human secreted polypeptide PRO1865, SEQ ID NO:384
US2003064449-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABM04669 standard; protein; 649 AA.
Human secreted polypeptide PRO1865, SEQ ID NO:384.
US2003068712-A1.
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Human secreted polypeptide PRO1865, SEQ ID NO:384.
US2003104541-A1.
05-JUN-2003.
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Human secreted polypeptide PRO1865, SEQ ID NO:384
US2003073174-A1.
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Human secreted polypeptide PRO1865, SEQ ID NO:384.
US2003104545-A1.
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Human secreted polypeptide PRO1865, SEQ ID NO.384
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Pred. No. 4.6e-11;
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Human secreted/transmembrane protein (PRO) #192.
US2003068775-A1.
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Best Local Similarity 22.3%;
RESULT 1461
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Length 649;

Score 309; DB 6; Pred. No. 4.6e-11;

Score 309; DB 6; Length 649; Pred. No. 4.6e-11; Score 309; DB 6; Length 649; Pred. No. 4.6e-11; Length 649; Score 309; DB 6; Length 649; Pred. No. 4.6e-11; Length 649; Length 649; Length 649; Length 649; Length 649; ABMI5703 standard; protein; 649 AA. Human secreted polypeptide PRO1865, SEQ ID NO:384. US2003068698-A1. ABM27357 standard; protein; 649 AA. Human secreted polypeptide PRO1865, SEQ ID NO:384. US2003068760-A1. ABM30102 standard; protein; 649 AA. Human secreted polypeptide PRO1865, SEQ ID NO:384. US2003068769-A1. ABM08688 standard; protein; 649 AA. Human secreted polypeptide PRO1865, SEQ ID NO:384 US2003068759-Al. ABM05638 standard; protein; 649 AA. Human secreted polypeptide PR01865, SEQ ID NO:384 ABO31051 standard; protein; 649 AA. Human secreted/transmembrane protein (PRO) #192. US2003064468-A1. 9.9%; Score 309; DB 6; 22.3%; Pred. No. 4.6e-11; 9.9%; Score 309; DB 6; 22.3%; Pred. No. 4.6e-11; ABO42288 standard; protein; 649 AA. Human secreted/transmembrane protein (PRO) #192. US2003049748-A1. Score 309; DB 6; Pred. No. 4.6e-11; Score 309; DB 6; Pred. No. 4.6e-11; 9.9%; Score 309; DB 6; 22.3%; Pred. No. 4.6e-11; Score 309; DB 6; Pred. No. 4.6e-11; ABO33040 standard, protein, 649 AA. Human PRO polypeptide #192. US2003064453-A1. 9.9%; Best Local Similarity 22.3%; Best Local Similarity 22.3%; RESULT 1497 Best Local Similarity 22.3%; RESULT 1490 Query Match Best Local Similarity 22.3%; RESULT 1492 9.9%; 03-APR-2003. (GETH ) GENENTECH INC. 10-APR-2003. (GETH ) GENENTECH INC. 03-APR-2003. (GETH ) GENENTECH INC. 10-APR-2003. (GETH ) GENENTECH INC. 13-MAR-2003. (GETH ) GENENTECH INC. 03-APR-2003. (GETH ) GENENTECH INC. (GETH ) GENENTECH INC. (GETH ) GENENTECH INC. GENENTECH INC. Best Local Similarity RESULT 1493 Best Local Similarity Best Local Similarity RESULT 1494 Query Match Best Local Similarity Best Local Similarity RESULT 1489 ID ABO30746 standard; US2003045700-A1. 06-MAR-2003. 10-APR-2003 10-APR-2003 Query Match Query Match Query Match Query Match

ABO38118 standard; protein; 649 AA

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DE Human secreted/transmembrane protein (PRO) #192.

PN US2003068765-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match

Best Local Similarity 22.3%; Pred. No. 4.6e-11;

RESULT 1498

DE Human PRO polypeptide #192.

PA (GETH) GENENTECH INC.

Query Match

Best Local Similarity 22.3%; Pred. No. 4.6e-11;

PAGRESULT 1499

ID ARMG6831 standard; protein; 649 AA.

RESULT 1499

ID ARMG6831 standard; Protein; 649 AA.

Best Local Similarity 22.3%; Pred. No. 4.6e-11;

RESULT 1499

ID ARMG6831 standard; protein; 649 AA.

DE Human secreted polypeptide PRO1865, SEQ ID NO:384.

PN US200308688-A1.

PN US200308677-A1.

PD Human secreted/transmembrane protein (PRO) #192.

PN US2003086776-A1.

PD U1-MAY-2003.

Query Match

PS UNG U1-MAY-2003.

PN US2003088767-A1.

PD U1-MAY-2003.

Query Match

PS U1-MAY-2003.

PN US20030876-A1.

PD U1-MAY-2003.

PN US20030876-A1.

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5: /cgn2_6/ptodata/1/pubpaa/USIO NEW PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/USIO NEW PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/USIO NEW PUB.pep:*
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Copyright (c) 1993 - 2006 Compugen Ltd
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US-11-135-855-37
US-11-137-047-47
US-11-147-047-47
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